

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6									
OM protein - protein search, using sw model										
Run on: November 3, 2005, 20:38:14 ; Search time 165 seconds	(without alignments)									
Perfect score: 2691	1 MRGELMVLVLRARALSL..... YAEVPEPSGHKEKGFMBAEQC 500									
Sequence: Scoring table: BL0SUM62	Gapext 0.5									
Searched: 2105692 seqs, 386760381 residues	Total number of hits satisfying chosen parameters: 2105692									
Minimum DB seq length: 0										
Maximum DB seq length: 2000000000										
Post-processing: Minimum Match 0*	Maximum Match 100*									
	Listing first 45 summaries									
Database : A_Geneseq_16Dec04;*										
1: geneseqD1980s;*										
2: geneseqD1990s;*										
3: geneseqD2000s;*										
4: geneseqD2001s;*										
5: geneseqD2002s;*										
6: geneseqD2003s;*										
7: geneseqD2003b;*										
8: geneseqD2004s;*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query	Match	Length	DB	ID	Description			
-	-	-	-	-	-	-	-	-	-	-
1	2691	100.0	500	5	ABBB90749		Abbb90749 Human Tum	XX	XX	XX
2	2691	100.0	500	6	ABBB90746		Abbb90746 Human Tum	XX	XX	XX
3	2691	100.0	500	7	ADII21063		Adii21063 Novel tum	XX	XX	XX
4	2691	100.0	500	8	ADH13230		Adh13230 Human mal	XX	XX	XX
5	2691	100.0	527	7	ADI21554		Adi21554 Novel hum	XX	XX	XX
6	2691	100.0	527	7	ADI21553		Adi21553 Novel hum	XX	XX	XX
7	2691	100.0	1002	5	ABB90723		Abb90723 Human Tum	XX	XX	XX
8	2691	100.0	1002	6	ABBB90723		Abbb90723 Human Tum	XX	XX	XX
9	2691	96.9	488	7	ADI21064		Adi21064 Novel hum	XX	XX	XX
10	2209	82.1	500	5	ABBB90783		Abbb90783 Mouse Tum	XX	XX	XX
11	2209	82.1	500	5	ABBB90729		Abbb90729 Mouse Tum	XX	XX	XX
12	2209	82.1	500	6	ABBB90736		Abbb90736 Mouse tum	XX	XX	XX
13	2209	82.1	500	6	ABBB90746		Abbb90746 Mouse tum	XX	XX	XX
14	2185	81.2	431	4	ABBB90740		Abbb90740 Tumour en	XX	XX	XX
15	2185	81.2	431	6	ABBB90734		Abbb90734 Human tum	XX	XX	XX
16	2007	74.6	400	3	AAB43131		Aab43131 Human ORF	XX	XX	XX
17	1326	49.3	351	8	ADRO9329		Adro9329 Human pro	XX	XX	XX
18	1295	48.1	499	4	AAB85396		Aab85396 Stem cell	XX	XX	XX
19	1295	48.1	499	6	ABO01430		Abo01430 Human ste	XX	XX	XX
20	1295	48.1	529	4	AAB85394		Aab85394 Stem cell	XX	XX	XX
21	1295	48.1	529	5	ABBB90734		Abbb90734 Human Tum	XX	XX	XX
22	1295	48.1	529	5	ABBB90726		Abbb90726 Human Tum	XX	XX	XX
23	1295	48.1	529	5	ABBB9349		Abbb9349 Human tra	XX	XX	XX
24	1295	48.1	529	5	ABG69157		Abg69157 Human ste	XX	XX	XX
25	1295	48.1	529	5	ABG69161		Abg69161 Human pro	XX	XX	XX

ALIGNMENTS

RESULT 1
ID ABBB90749 standard; protein; 500 AA.
AC ABBB90749;
XX DT 30-MAY-2002 (first entry)
XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cyostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antangiogenic; tumour; neoangiogenesis; vascularised tumour; KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; KW psoriasis.
XX OS Homo sapiens.
XX PN WO200210217-A2.
XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US024031.

SUMMARIES

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

Claim 1; Page 202-291856/33. N-P5DB; ABL92103.

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

WPI; 2002-291856/33.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cyostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

CC retinopathy, rheumatoid arthritis and psoriasis Human, mouse and rat TEM
 CC genes and the encoded proteins (ABL9205-ABL92141 and ABB0721-ABL90789)
 CC are disclosed, as are marker oligonucleotide sequences: tumour
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 (PEM) ABL91901-ABL91995

XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 5; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.2e-249; Gaps 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MRGEWILVLYLREARALSPQPGAGHDGPMSGWAAKSTVGNNRRAESPGHVSSEPR 60
 Db 1 MRGEWILVLYLREARALSPQPGAGHDGPMSGWAAKSTVGNNRRAESPGHVSSEPR 60

Qy 61 TQLSDLGTTLAMDTLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQTK 120

Db 61 TQLSDLGTTLAMDTLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQTK 120

Qy 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

Db 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

Qy 181 NENPGYSDINSTVYYFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 240

Db 181 NENPGYSDINSTVYYFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 240

Qy 241 SVPESSSSQPVKTGLSDATMILNSPDYPSRSRIPEFYRIELDPSVTSMSAVEFTPP 300

Db 241 SVPESSSSQPVKTGLSDATMILNSPDYPSRSRIPEFYRIELDPSVTSMSAVEFTPP 300

Qy 301 LPTCLOQRHSCDACHMSDLTFCNSWCHVLRQCSGFDRYTFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 360

Db 301 LPTCLOQRHSCDACHMSDLTFCNSWCHVLRQCSGFDRYTFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 360

Qy 361 DEDHDSASPDTSFSPSYDGLLTTSSSLFDLSDLTEDDTKLNPYAGDGTLQNNLSPKTKT 420

Db 361 DEDHDSASPDTSFSPSYDGLLTTSSSLFDLSDLTEDDTKLNPYAGDGTLQNNLSPKTKT 420

Qy 421 PVLHLGTTIVGTVLAVLVAAILLAGTYINGHPTSNALFLERRPHWPMKFRSHPDIST 480

Db 421 PVLHLGTTIVGTVLAVLVAAILLAGTYINGHPTSNALFLERRPHWPMKFRSHPDIST 480

Qy 481 YAEVEPSGHKEKEGMNEAQQC 500

Db 481 YAEVEPSGHKEKEGMNEAQQC 500

RESULT 2

ABU54456 standard; protein; 500 AA.

AC ABU54456;

XX DT 12-MAR-2003 (first entry)

XX Human tumour endothelial marker TEM 17.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;

XX Tumour endothelial marker; normal endothelial marker; PEM;

XX pan-endothelial marker; polycystic kidney disease; porriasis;

XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;

XX neoangiogenesis; immune response; cytotoxic; antidiabetic;

XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic;

XX Homo sapiens.

DB 705 WO200283874-A2.

PN 733 24-OCT-2002.

PD XX

PF 10-APR-2002; 2002WO-US008253.
 XX

PR 11-APR-2001; 2001US-022850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX

(UYJO) UNIV JOHNS HOPKINS.
 XX

PA Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX

PI WPI: 2003-093016/08.

DR N-PSDB; ABX72028.

XX New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors or polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

XX Disclosure; Page 221-222; 374pp; English.

XX The present invention relates to a novel method for the isolation of endothelial cells (ECS), and the identification of genes expressed in normal and tumour ECS. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECS. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention.

XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.2e-240; Gaps 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0;

PS 0; Gaps 0;

CC The present invention relates to a novel method for the isolation of

CC endothelial cells (ECS), and the identification of genes expressed in

CC normal and tumour ECS. Tumour endothelial marker (TEM), normal

CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

CC identified in human ECS. The human EC marker proteins and the

CC polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

CC useful for inhibiting neangiogenesis or tumour angiogenesis, for

CC inducing an immune response to tumour endothelial cells in a patient, or

CC for identifying candidate drugs for treating tumours. The present

sequence represents a human TEM or NEM protein of the invention.

XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 6; Length 500;

Best Local Similarity 100.0%; Pred. No. 3.2e-240; Gaps 0;

Matches 500; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

CC Query 1 MRGFLWILVLYLREARALSPQPGAGHDGPMSGWAAKSTVGNNRRAESPGHVSSEPR 60

Db 1 MRGEWILVLYLREARALSPQPGAGHDGPMSGWAAKSTVGNNRRAESPGHVSSEPR 60

CC Query 61 TQLSDLGTTLAMDTLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQTK 120

Db 61 TQLSDLGTTLAMDTLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQTK 120

CC Query 61 TQLSDLGTTLANDLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQVK 120

Db 61 TQLSDLGTTLANDLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQVK 120

CC Query 61 TQLSDLGTTLANDLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQVK 120

Db 61 TQLSDLGTTLANDLPDNTRVVEDNISYYVSPLYGSEPHRELWDAEANRSQVK 120

CC Query 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

Db 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

CC Query 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

Db 121 IHTILSNTHQASRVLSPDFPYCHPLRQITIATGGFIFMGDYTHRMLTATOYVAPLMA 180

CC Query 181 NENPGYSDINSTVYYFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 240

Db 181 NENPGYSDINSTVYYFDNGTUVYDVKVQDHYVQLQGWEDKGSTFOQAALHHDRIVPKEYFIM 240

CC Query 241 SVPBISSSHOPVKTGSLDARMILNPSDVPESSRSIFEVYHRIELDPSKVTMSAVERFTP 300

Db 241 SVPBISSSHOPVKTGSLDARMILNPSDVPESSRSIFEVYHRIELDPSKVTMSAVERFTP 300

CC Query 301 LPTCLQHRSQDCAMSDSLTFNCSCMCHVLRQCSGFDRYFQEWMDYGCADBAEGMCEDFQ 360

Db 301 LPTCLQHRSQDCAMSDSLTFNCSCMCHVLRQCSGFDRTFQEWMDYGCADBAEGMCEDFQ 360

CC Query 361 DEHDIDASPDTSFSPYDQGDLTTTSSSLFDSLTTTBDDKUNPYAGGDGLQNNLSPKTGT 420

Db 361 DEHDIDASPDTSFSPYDQGDLTTTSSSLFDSLTTTBDDKUNPYAGGDGLQNNLSPKTGT 420

CC Query 421 PVHIGTIVGVILVLAAILAGYINCHTPSNALPFIERRPHWPMKFRSHPDHST 480

Db 421 PVHIGTIVGVILVLAAILAGYINCHTPSNALPFIERRPHWPMKFRSHPDHST 480

CC Query 481 YAEVEPSGHKEKEGMNEAQQC 500

Db 481 YAEVEPSGHKEKEGMNEAQQC 500

CC Query 481 YAEVEPSGHKEKEGMNEAQQC 500

Db 481 YAEVEPSGHKEKEGMNEAQQC 500

cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia such as breast cancer, ovarian cancer, gastric cancer, colon cancer, oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell lung cancer. The polynucleotides and polypeptides defined in the specification, antisense polynucleotides and polypeptides targeting the polynucleotides, antibodies targeting either one of the polynucleotides or polypeptides, and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of the invention.

xx Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 8; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.2e-24; Mismatches 0; Indels 0; Gaps 0;
Matches 500; Conservative 0; N -PDB; ADI21334.

Qy 1 MRGEWILWVLRERARALSPQPAGHDGPGSGWAAKCTVRGNRRAEBSPGHVESEPR 60
Db 1 MRGEWILWVLRERARALSPQPAGHDGPGSGWAAKCTVRGNRRAEBSPGHVESEPR 60
Qy 61 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 120
Db 61 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 120
Qy 121 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 180
Qy 181 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 240
Db 181 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 240
Qy 241 SVPEITSSQHPVKYGLSDAMILNCSMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 300
Db 241 SVPEITSSQHPVKYGLSDAMILNCSMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 300
Qy 301 LPTCLQHRSQDAMCSLDLTFNCSCMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSQDAMCSLDLTFNCSCMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 360
Qy 361 DEDHDSASPDTSESPPDYDGLTTSSSLFLDSLITEDDTKLNPYACGDIQNLSPKTC 420
Db 361 DEDHDSASPDTSESPPDYDGLTTSSSLFLDSLITEDDTKLNPYACGDIQNLSPKTC 420
Qy 422 PVLHGTIVGVTLAVLVAATLAGIYINGHPTNSAALPFTERRPHWPMKFRSHPDIST 480
Db 422 PVLHGTIVGVTLAVLVAATLAGIYINGHPTNSAALPFTERRPHWPMKFRSHPDIST 480
Qy 481 YAEVPSGHEKEGMFMEAQC 500
Db 481 YAEVPSGHEKEGMFMEAQC 500

RESULT 5
AD121554 standard; protein; 527 AA.
ID AD121554
XX AC ADI21554;
XX DT 15-APR-2004 (first entry)
DE Novel human polypeptide #33.
XX forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
XX

xx Homo sapiens.
OS XX
PN WO2003025148-A2.
CC XX
PD 27-MAR-2003.
CC XX
PF 19-SEP-2002; 2002WO-US029964.
CC XX
PR 19-SEP-2001; 2001US-0323739P.
PR 13-SEP-2002; 2002US-03323739.
XX
(HYSE-) HYSEQ INC.
PA XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX
DR WPI; 2003-354603/33.
N-PDB; ADI21334.
XX
PT New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
XX
PS Example 3; SEQ ID NO 805; 156pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight marker, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are markers for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human polypeptide.
XX
SQ Sequence 527 AA;
Query Match 100.0%; Score 2691; DB 7; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.5e-249; Mismatches 0; Indels 0; Gaps 0;
Matches 500; Conservative 0; N -PDB; ADI21334.

Qy 1 MRGEWILWVLRERARALSPQPAGHDGPGSGWAAKCTVRGNRRAEBSPGHVESEPR 60
Db 28 MRGEWILWVLRERARALSPQPAGHDGPGSGWAAKCTVRGNRRAEBSPGHVESEPR 87
Qy 61 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 120
Db 61 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 120
Qy 88 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 147
Db 88 TQLSDQDGCGTLMNDTLPLDRTRVVEDNHSYYVSRLYGPSEPHSERLWYDVAANRSQVK 147
Qy 121 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 180
Qy 148 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 207
Db 148 IHTILSNTHQASRVVLSTDFPFYGHPLQQTIAATGGFIFMGDVYTHRMLTATQYVAPLMA 207
Qy 181 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 240
Db 181 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 240
Qy 208 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 267
Db 208 NENQYSDISTVQYFDNGTIPVQDHLVNLQGDWDXGSSTFOQALHHQDRIVPAYKEIPM 267

Qy 241 SUPRISSSQHPVKTGQSLDAFMILNPSDVPESRRSIFYHRFLDPSKTVMSAVEFTP 300
Db 268 SUPRISSSQHPVKTGQSLDAFMILNPSDVPESRRSIFYHRFLDPSKTVMSAVEFTP 327
Qy 301 LPTCLQHRSQDAMCSLDLTFNCSCMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 360
Db 328 LPTCLQHRSQDAMCSLDLTFNCSCMCHVLCRCSGGFDRYQEWMDYGAQAEGRMCEDFQ 387

QY	361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLLTEDDTKLNPYAGGDGTQNNLSPKTGCT 420	XX	SQ Sequence 527 AA;
Db	388 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLLTEDDTKLNPYAGGDGTQNNLSPKTGCT 447	Query Match 100.0%; Score 2691; DB 7; Length 527;	
QY	421 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTNSNALFPIERRPHWPMKFRSHPDIST 480	Best Local Similarity 100.0%; Pred. No. 3 5e-249; Indels 0; Gaps 0;	
Db	448 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTNSNALFPIERRPHWPMKFRSHPDIST 507	Matches 500; Conservative 0; Missmatches 0;	
QY	481 YAEVPSGHEKEGMNEAQ C 500	QY 1 MREGEMLLVLVLRERARALSPQPGAGHDGPGSWAAKGTVGRGNMRAESPGHSEPR 60	
Db	508 YAEVPSGHEKEGMNEAQ C 527	Db 28 MRGEWLVLVLRERARALSPQPGAGHDGPGSWAAKGTVGRGNMRAESPGHSEPR 87	
RESULT 6			
AD121553	ID AD121553 standard; protein; 527 AA.	QY 61 TQLSDLGCGSTLANDTLPDNTRTRYEDNHSYXYSSLYGSEPHSRELWDVAEANSQVK 120	
XX	XX	Db 88 TQLSDLGCGSTLANDTLPDNTRTRYEDNHSYXYSSLYGSEPHSRELWDVAEANSQVK 147	
AC	AD121553	QY 121 IHTILSNTRQAISRVLSPDPFPYGHPLRQITATGGFPMDVYHRLMTAQVAPLMA 180	
DT	15-APR-2004 (first entry)	Db 148 IHTILSNTRQAISRVLSPDPFPYGHPLRQITATGGFPMDVYHRLMTAQVAPLMA 207	
XX	Novel human polypeptide #32.	QY 181 NFNPGSDNSITVVYFDNGTVFVYQMDHYLQGWEDKGSTFOAHLHHDRGIVFAYKEIPM 240	
DB		Db 208 NFNPGSDNSITVVYFDNGTVFVYQMDHYLQGWEDKGSTFOAHLHHDRGIVFAYKEIPM 267	
XX	forensic; nutritional source; damaged tissue; diseased tissue;	QY 241 SVPEISSLSSQHPVKTGLSDAFMILNPSDVPESRRSIFYHRIELDPSKVTMSAVEFTP 300	
KW	myeloid cell disorder; lymphoid cell disorder;	Db 268 SVPEISSLSSQHPVKTGLSDAFMILNPSDVPESRRSIFYHRIELDPSKVTMSAVEFTP 327	
KW	bone cartilage tissue; growth; tendon tissue growth;	QY 301 LPTCLQHRSQDCAMS SDLTFNCSCWHLQRCSSGFDYRQEWNMDYGCABAEGRMCDFQ 360	
KW	ligament tissue growth; nerve tissue growth; regeneration; wound healing;	Db 328 LPTCLQHRSQDCAMS SDLTFNCSCWHLQRCSSGFDYRQEWNMDYGCABAEGRMCDFQ 387	
KW	tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.	QY 361 DEHDIDASPDTSFSPYDGLDTTISLFDDSLTEDTKLNPYAGGDGLQNNLSPKTGCT 420	
XX	Homo sapiens.	Db 388 DEHDIDASPDTSFSPYDGLDTTISLFDDSLTEDTKLNPYAGGDGLQNNLSPKTGCT 447	
PN	WO2003025148-A2.	QY 421 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTNSNALFPIERRPHWPMKFRSHPDHST 480	
XX	27-MAR-2003.	Db 448 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTNSNALFPIERRPHWPMKFRSHPDHST 507	
PD		QY 481 YAEVPSGHEKEGMNEAQ C 500	
XX	19-SEP-2002; 2002WO-US029964.	Db 508 YAEVPSGHEKEGMNEAQ C 527	
PF			
XX	19-SEP-2001; 2001US-0323739P.		
PR	13-SEP-2002; 2002US-00323739.		
PA	(HYSEQ INC.)		
XX	Tang YT, Abundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J, Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D; Haley-Vicente D;	RESULT 7	
WPI	2003-354603/33.	ABB90723 ID ABB90723 standard; protein; 1002 AA.	
XX	DR N-PSDB; ADI12133.	XX	
DR		AC ABB90723;	
XX		DT 30-MAY-2002 (first entry)	
XX		XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.	
PT		XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;	
PT		XX normal endothelial marker; pan-endothelial marker; immunostimulant;	
PT		XX antiangiogenic; tumour; neangiogenesis; vascularised tumour;	
XX		XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; Homo sapiens.	
PS	Example 3; SEQ ID NO 804; 156pp; English.	OS OS	
PA		XX WO200210217-A2.	
XX	The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement.	XX PD 07-FEB-2002.	
CC	XX Example 3; SEQ ID NO 804; 156pp; English.	XX PF 01-AUG-2001; 2001WO-US024031.	
CC	XX New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.	XX PR 02-AUG-2000; 2000US-0222593P.	
CC	XX The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcer, and in treating cancer. The present sequence represents the amino acid sequence of a novel human polypeptide.	XX PR 11-AUG-2000; 2000US-0224360P.	
CC	XX	XX PR 11-APR-2001; 2001US-0282850P.	
CC	XX PA (UYJO) UNIV JOHNS HOPKINS.	XX PA	

XX	PI St Croix B, Kinzler KW, Vogelstein B;	XX	DT 12-MAR-2003 (first entry)
XX	DR; 2002-291056-33.	XX	DE Human tumour endothelial marker TEM 8.
XX	An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.	XX	KW Human; endothelial cell; BC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; panendothelial marker; polycystic kidney disease; psoriasis; KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; KW neangiogenesis; immune response; cytosstatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX	Disclosure; Page 125-128; 331pp; English.	XX	KW XX
CC	The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB07032, ABB0740, ABB0749, ABB0750 and ABB0769. The antibodies which bind to TEM proteins have cytotoxic, immunosuppressive and antiangiogenic activity.	OS Homo sapiens.	XX
CC	They are useful for inhibiting tumour growth, neangiogenesis in subjects bearing a vascularised tumor, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92025-ABL9211 and ABL92789) are disclosed, as are marker Oligonucleotide sequences; tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995	XX	PN WO20028874-A2.
XX	Sequence 1002 AA;	XX	XX
Qy	Query Match 100.0%; Score 2651; DB 5; Length 1002; Best Local Similarity 100.0%; Pred. No. 9-5e-249; Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	DR WPI; 2003-09-016/08.
Db	1 MRGEMLLVLVYLREARALSPQPAGHDEGPSSGWAARKGVGNRRARESPGHVSEPR 60 503 TQLSQDGGTLAMDTLPDNTRVYEDNTNYYVSPLYGPSEPHSRELWYDVAEANSQVK 120	XX	N-PDB; ABX72003.
Qy	61 TQLSQDGGTLAMDTLPDNTRVYEDNTNYYVSPLYGPSEPHSRELWYDVAEANSQVK 120 563 TQLSQDGGTLAMDTLPDNTRVYEDNTNYYVSPLYGPSEPHSRELWYDVAEANSQVK 622	XX	PT New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
Db	623 IHTILSNTHQASRVVLSDFPPYGHPLRQITIATGGFIFMGDVTHRMLTATQVAPIMA 180 623 IHTILSNTHQASRVVLSDFPPYGHPLRQITIATGGFIFMGDVTHRMLTATQVAPIMA 682	XX	PT Disclosure; Page 122-124; 374pp; English.
Qy	681 NFNPQGYSDNSTVYYFDNGTVFVQMDHVTQGLWKGSDFTFOAALHHDRGIVFAKEIENM 240 683 NFNPQGYSDNSTVYYFDNGTVFVQMDHVTQGLWKGSTTFOAALHHDRGIVFAKEIENM 742	XX	CC The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker genes and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. They are also useful for inhibiting neangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
Db	741 SVPETSSSHQPVKGLSDAFMLNLPSPDVYEPESRRRSIIFYTHRIELDPSKVTSMSAVERFP 300 743 SVPETSSSHQPVKGLSDAFMLNLPSPDVYEPESRRRSIIFYTHRIELDPSKVTSMSAVERFP 802	XX	CC Sequence 1002 AA;
Qy	743 SVPETSSSHQPVKGLSDAFMLNLPSPDVYEPESRRRSIIFYTHRIELDPSKVTSMSAVERFP 802 301 LPTCLQRSCDACKMSDLTFCNSWCHVLQRCSGGPDRYQEWMDYGAQEAEGRMCEDFQ 360 803 LPTCLQRSCDACKMSDLTFCNSWCHVLQRCSGGPDRYQEWMDYGAQEAEGRMCEDFQ 862	XX	CC Query Match 100.0%; Score 2691; DB 6; Length 1002; Best Local Similarity 100.0%; Pred. No. 9-5e-249; Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	361 DEDHDASPDTSFSFSPYDGDLTTSSSLFDTSLLTEDDTKLNPYAGDGQLQNNLSPKTGT 420 863 DEDHDASPDTSFSFSPYDGDLTTSSSLFDTSLLTEDDTKLNPYAGDGQLQNNLSPKTGT 922	XX	Qy 1 MRGEMLLVLVYLREARALSPQPAGHDEGPSSGWAARKGVGNRRARESPGHVSEPR 60 503 MRGEMLLVLVYLREARALSPQPAGHDEGPSSGWAARKGVGNRRARESPGHVSEPR 562
Qy	863 DEHDASPDTSFSFSPYDGDLTTSSSLFDTSLLTEDDTKLNPYAGDGQLQNNLSPKTGT 922 421 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTSNALFIERPHWPMKFRSHPDHST 480 923 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTSNALFIERPHWPMKFRSHPDHST 982	Db	61 TQLSDLGCGTLLAMDTLPDNTRVYEDNTNYYVSPLYGPSEPHSRELWYDVAEANSQVK 120 563 TQLSDLGCGTLLAMDTLPDNTRVYEDNTNYYVSPLYGPSEPHSRELWYDVAEANSQVK 622
Db	923 PVHLGTTIVGIVLAVLVAAILLAGIYINGHPTSNALFIERPHWPMKFRSHPDHST 982 481 YAEVEPSGHEKEGFMEAQOC 500	Qy	623 IHTILSNTHQASRVVLSDFPPYGHPLRQITIATGGFIFMGDVTHRMLTATQVAPIMA 180 683 NFNPQGYSDNSTVYYFDNGTVFVQMDHVTQGLWKGSDFTFOAALHHDRGIVFAKEIENM 742
Qy	481 YAEVEPSGHEKEGFMEAQOC 500 983 YAEVEPSGHEKEGFMEAQOC 1002	Db	181 NFNPQGYSDNSTVYYFDNGTVFVQMDHVTQGLWKGSDFTFOAALHHDRGIVFAKEIENM 240 683 NFNPQGYSDNSTVYYFDNGTVFVQMDHVTQGLWKGSDFTFOAALHHDRGIVFAKEIENM 742
AC	ABUS4430; ABUS4430 standard; protein; 1002 AA.	Qy	241 SVPEISSQHPVKGLSDAFMLNLPSPDVYEPESRRRSIIFYTHRIELDPSKVTSMSAVERFP 300

RESULT 8

ABUS4430

ID ABUS4430

XX standard; protein; 1002 AA.

AC ABUS4430;

XX	PR 02-AUG-2000; 2000US-0222599P.	RESULT 11
PR 11-AUG-2000; 2000US-0224360P.	ABB90729	ID ABB90729 standard; protein, 500 AA.
PR 11-APR-2001; 2001US-0282850P.	XX	
XX	(UWJO) UNIV JOHNS HOPKINS.	AC ABB90729;
XX	PI St Croix B, Kinzler KW, Vogelstein B;	XX
XX	DR WPI: 2002-291856/33.	DT 30-MAY-2002 (first entry)
XX	DR -N-PSDB; ABL92136.	XX
XX	An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.	XX
PT Disclosure: Page 301-302; 331pp; English.	XX	
CC The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL9211 and ABL90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91995-ABL92041 and ABL92143-ABL9191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995	XX	
CC Sequence 500 AA:	XX	OS Mus musculus.
CC	XX	XX
CC	XX	PN WO200210217-A2.
CC	XX	XX
CC	XX	PD 07-FEB-2002.
CC	XX	PF 01-AUG-2001; 2001WO-US024031.
CC	XX	PR 02-AUG-2000; 2000US-0222599P.
CC	XX	PR 11-AUG-2000; 2000US-0224360P.
CC	XX	PR 11-APR-2001; 2001US-0282850P.
CC	XX	PA (UWJO) UNIV JOHNS HOPKINS.
CC	XX	PA St Croix B, Kinzler KW, Vogelstein B;
CC	XX	XX
CC	XX	DR WPI: 2002-291856/33.
PT An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.	XX	DR
PT Disclosure: Page 146-147; 331pp; English.	XX	PT
CC The invention relates to an isolated molecule comprising an antibody to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL9211 and ABL90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91995-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995	CC	
CC Sequence 500 AA:	XX	CC
Query Match 82.1%; Score 2209; DB 5; Length 500;	XX	CC
Best Local Similarity 81.6%; Pred. No. 7e-203; Mismatches 46; Indels 2; Gaps 2;	XX	CC
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;	XX	CC
Qy 1 MRGELWLL-VVLRDARALSPQPGAGHDEPGCGSCWAAKCTVQRNARRARESPHNSEND 59	Db 1 MRAQLWLQLLRLGRARALSPATPGHNEQDQSANTALKTROQWSRRESPSPAQVLKEG 60	CC
Qy 60 RTQLSQDLGGCTLANDTLDPNRTRVVEDHNSYYVSRLYGPSEPHSRELMDVAEANRSVY 119	Db 61 KTQLSQDLGGCSLADTLDPNRTRVVEDHNYYSRVPGKQSVFGEKOSQDLYTDLVANRSVY 120	CC
Qy 120 KIHTLISNTNHTRQASRVLSDFPFYGHPLRQITIATGGFTFMGDTYTHRLMTATQVAPLM 179	Db 121 KIHLISSLRQASRVLSDFPFYGHPLRQITIATGGFTFMGDLMLHRLMTATQVAPLM 180	CC
Qy 180 ANFNGYSNDSTNVYFEDNGTYVNWQDHVYLQHNGDKSGFTFOAHLHNGRIVYAKBTP 239	Db 181 ANFNGYSNDSTVAFDNGTYVWQDHVYLQDRDGSGFTFOAHLHRGRIVYGYKETP 240	CC
Qy 240 MSVPBTSQSHPVKGGLSDAFMILNPSPDVPESSRSIPEYHRFLDPSKVTSMSAVERT 299	Db 241 MAVFDISSAQPVVKPGLSDAFMILNPSPDVPESSRSIPEYHRFLDPSKVTSMSAVERT 300	CC
Qy 300 PLPTCLQHRSQCDACMSSDLTFCNCMSWVQPGAGHDEPGCGSCWAAKGTVDRCWNRARESPGHVSEPD 359	Db 301 PLPTCLQHQSCDTCVSSNLTFNCSCWVLRQCSSGFDRQEMTYGQABGKTCEP 360	CC
Qy 360 QDEDBHDSSASDTSFSPYDGLTTSSSLIDSLTTEDDPKLNYPAGGDQJONNLSPKTG 419	Db 361 QDDSHYSASPSSSFPGD-STTSSSLIDSLTTEDDPKLNYPAGGDQJONNLSPKTG 419	CC
Qy 420 TPVHGTGTVIGIVLAVLAILAGTYINCHPTNSAALPIERPHWAMKFRSHPDES 479	Db 420 PPVHGTGTVIGIVLAVLAILAGTYINCHPTNSAALPIERPHWAMKFRSHPDES 479	CC
Qy 480 TAAVEVPSSHEKEGMNEABOC 500	Db 480 TYTEVEPSSHEKEGFYEA3QC 500	CC
Qy 120 KIHLISSLRQASRVLSDFPFYGHPLRQITIATGGFTFMGDTYTHRLMTATQVAPLM 179	Db 121 KIHLISSLRQASRVLSDFPFYGHPLRQITIATGGFTFMGDTYTHRLMTATQVAPLM 180	CC

Query Match 82.1%; Score 2209; DB 5; Length 500;
 Best Local Similarity 81.6%; Pred. No. 7e-203;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;
 Qy 1 MRGELWLL-VVLRDARALSPQPGAGHDEPGCGSCWAAKCTVQRNARRARESPHNSEND 59
 Db 1 MRAQLWLQLLRLGRARALSPATPGHNEQDQSANTALKTROQWSRRESPSPAQVLKEG 60
 Qy 60 RTQLSQDLGGCTLANDTLDPNRTRVVEDHNSYYVSRLYGPSEPHSRELMDVAEANRSVY 119
 Db 61 KTQLSQDLGGCSLADTLDPNRTRVVEDHNYYSRVPGKQSVFGEKOSQDLYTDLVANRSVY 120
 Qy 120 KIHTLISNTNHTRQASRVLSDFPFYGHPLRQITIATGGFTFMGDTYTHRLMTATQVAPLM 179
 Db 121 KIHLISSLRQASRVLSDFPFYGHPLRQITIATGGFTFMGDLMLHRLMTATQVAPLM 180
 Qy 180 ANFNGYSNDSTNVYFEDNGTYVNWQDHVYLQHNGDKSGFTFOAHLHNGRIVYAKBTP 239
 Db 181 ANFNGYSNDSTVAFDNGTYVWQDHVYLQDRDGSGFTFOAHLHRGRIVYGYKETP 240
 Qy 240 MSVPBTSQSHPVKGGLSDAFMILNPSPDVPESSRSIPEYHRFLDPSKVTSMSAVERT 299
 Db 241 MAVFDISSAQPVVKPGLSDAFMILNPSPDVPESSRSIPEYHRFLDPSKVTSMSAVERT 300
 Qy 300 PLPTCLQHRSQCDACMSSDLTFCNCMSWVQPGAGHDEPGCGSCWAAKGTVDRCWNRARESPGHVSEPD 359
 Db 301 PLPTCLQHQSCDTCVSSNLTFNCSCWVLRQCSSGFDRQEMTYGQABGKTCEP 360
 Qy 360 QDEDBHDSSASDTSFSPYDGLTTSSSLIDSLTTEDDPKLNYPAGGDQJONNLSPKTG 419
 Db 361 QDDSHYSASPSSSFPGD-STTSSSLIDSLTTEDDPKLNYPAGGDQJONNLSPKTG 419
 Qy 420 TPVHGTGTVIGIVLAVLAILAGTYINCHPTNSAALPIERPHWAMKFRSHPDES 479
 Db 420 PPVHGTGTVIGIVLAVLAILAGTYINCHPTNSAALPIERPHWAMKFRSHPDES 479
 Qy 480 TAAVEVPSSHEKEGMNEABOC 500
 Db 480 TYTEVEPSSHEKEGFYEA3QC 500

XX	PF	10-APR-2002;	2002W0-US008253.		Db	480 TYTEVEPSGHEKEGFVAAEQC 500
XX	PR	11-APR-2001;	2001US-0282850P.			RESULT 14
PR	06-FEB-2002;	2002US-0354262P.				AAB85400
XX	PA	(UYJO)	UNIV JOHNS HOPKINS .			ID AAB85400 standard; protein; 431 AA.
XX	P1	Carson-Walter B,	St Croix B,	Kinzler KW,	Vogelstein B;	XX
XX	DR	WPI; 2003-093016/08.				AC AAB85400;
XX	DR	N-PSDB;	ABX72061.			
XX	PT	New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumor, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.				XX
PS	Disclosure:	Page 339-340; 374pp; English.				XX
XX	The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumors as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumors. The present sequence represents a mouse TEM protein			XX		
SQ	Sequence 500 AA;					XX
	Query Match	82.1%;	Score 2209;	DB 6;	Length 500;	
	Best Local Similarity	81.6%;	Pred. No. 7e-203;			
	Matches 409;	Conservative 46;	Mismatches 44;	Indels 2;	Gaps 2;	
Qy	1	MRGEIWLLL-VLVLREARALSPQEAGAHDGPGCSWAAGKTVGRWNRRARESPGHVSEED	59			XX
Db	1	MRAQLWLLQQLLRLGAAARALSPATPAGHNEQGDSAWTAKTRQGMWSRRRESPAQVLKEG	60			XX
Qy	60	RTOLOSDQDGGCTLAMDTPDNTRTRYEDNHSSYYRSRLYCGSEPHSRLEWVDVAEANRSCV	119			XX
Db	61	KTQISQDQLGCGSLADTLPNTRTRYEDNHYYRSRVGRGXOSQDILWDLVANRSHV	120			CC
Qy	120	KIHTLISNTHRQASRVLSPVTVFDNGTVFVQWDHVTQGLMEDKGSPFTFOALHHGRIPAYKEP	179			CC
Db	121	KIHRLLSSHRQASRVLSPVTVFDNGTVFVQWDHVTQGLMEDKGSPFTFOALHHGRIPAYKEP	180			CC
Qy	180	ANFNGYSNDSTVVYFDNGTVFVQWDHVTQGLMEDKGSPFTFOALHHGRIPAYKEP	239			CC
Db	181	ANFNGYSNDSTVVYFDNGTVFVQWDHVTQGLMEDKGSPFTFOALHHGRIPAYKEP	240			CC
Qy	240	MSVPEIISSQHPVKTGLSDAFMLINPSDVPEPESRRTSIEYHR1ELDPSKVTSMSAVET	299			CC
Db	241	MAVDIASSAHPVKAGLSDAFMILNSSPEPESQRTTIEYHR1ELDPSKVTSMSAVET	300			XX
Qy	300	PLPTCLQHRSQCDACMSDTFNCSCWCHVYLQRCSSGFDRYRQENMDYGCQAEGRMCF	359			SQ Sequence 431 AA;
Db	301	PLPTCLQHRSQCDTCVSSNLTFCNSCWWVYLQRCSSGFDRYRQENMDYGCQAEGRMCF	360			
Qy	360	QDEDHDASDTSFPPYDGLTTSSLFDSLTDKLNPYAGGDQLQNLSPTKG	419			Query Match 81.2%; Score 2185;
Db	361	QDDSHYASDSSPSPFNGD-STTSSSLFDSLTDKLNPYAGGDQLPDHSSPSKKG	419			Best Local Similarity 95.2%; Pred. No. 1.1e-200;
Qy	420	TPVHLGTTIVGVLAVLVAIAITLAGIYINCHPTSNAAFLPTTERRPHWDMKFRSHPD	479			Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;
Db	420	PPVHLGTTIVGVLAVLVAIAITLAGIYINCHPTSNAAFLPTTERRPHWDMKFRSHPD	479			Qy 72 LAMDTLPDRTRVBDNISYYVSRLYCGSEPHSRLEWVDVAEANRSGVKTHTLSNTHQ 131
Qy	480	TYAEVEPSGHEKEGFMEAOEC 500				Db 1 LAMDTLPDRTRVBDNISYYVSRLYCGSEPHSRLEWVDVAEANRSGVKTHTLSNTHQ 60
Qy	192	VVYFDNGTIVFVWVONDHVYLGWEDKGSPFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP				Qy 132 ASRVVLSDFPPYCHPLRQITIATGFLFMGDVIRHMTATOVAPMANFNPGYSDNST 191
Qy	192	VVYFDNGTIVFVWVONDHVYLGWEDKGSPFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP				Db 61 ASRVVLSDFPPYCHPLRQITIATGFLFMGDVIRHMTATOVAPMANFNPGYSDNST 120

Db	121 VVYFDNGTGVVVQMDHIVYLLQCGWEDKGCSFTFOAALHHDRIVPAYKBIPMSVPBISSSQHP	180	CC the polynucleotide is useful for treating a subject in need to inhibit the activity or expression of stem cell growth factor-like polypeptide.
Qy	252 VKTGLSDAFMILNPSPDVPSRRSIFFEVHRIELDPSKTSMSAVFTLPLTCLOHRSQCD	311	CC The new polypeptide or polynucleotide is particularly useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types. In particular, the polypeptide or polynucleotide is useful for treating leukaemia, haemophilia, osteoporosis, osteoarthritis, anaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g. multiple sclerosis, systemic lupus erythematosus, graft-versus-host disease or allergies), cancers or degenerative diseases (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease or amyotrophic lateral sclerosis) or for generating new tissues and organs that may aid patients in need of transplanted tissues. The polynucleotide may also be used in gene therapy for the treatment of these diseases. The new polypeptide or polynucleotide is also useful in diagnostic or research methods. The present sequence represents the human tumour endothelial marker 7 precursor protein
Db	181 VRTGGLSDAFTNPSPDVPSRRSIFFEVHRIELDPSKTSMSAVFTLPLTCLOHRSQCD	240	CC present sequence represents the human tumour endothelial marker 7 precursor protein
Qy	312 ACMSSDLTENCSWCHVLQRQSSGFDYRQEW-MDYGCAQAEGRMCEDQD-----ED	363	CC
Db	241 ACMSSDLTENCSWCHVLQRQSSGFDYRQEW-MDYGCAQAEGRMCEDQD-----ED	294	CC
Qy	364 HDSASPDTSSSPYGDLTSSFLDSLTEDDTKLNPVAGGDLQNLNSPKTKGTGTPH	423	CC
Qy	295 TTSASPDTSSSPYGDLTSSFLDSLTEDDTKLNPVAGGDLQNLNSPKTKGTGTPH	354	CC
Db	424 LGTIVGIVLVVAVIILLAGIYINGHPTSNAAFFIERRPHWPMKFRSHPDHSTYAB	483	CC
Qy	424 LGTIVGIVLVVAVIILLAGIYINGHPTSNAAFFIERRPHWPMKFRSHPDHSTYAB	414	CC
Db	355 LGTIVGIVLVVAVIILLAGIYINGHPTSNAAFFIERRPHWPMKFRSHPDHSTYAB	414	CC
Qy	484 VEPSGEKEKGFMEEAQC 500	431	CC
Db	415 VEPSGEKEKGFMEEAQC 431	431	CC
Qy	431 AA;	431	CC
Db	Sequence 431 AA;	431	XX
Qy	Query Match Score 2185; DB 6; Length 431;	431	XX
Db	Best Local Similarity 95.2%; Pred. No. 1.1e-200; Mis matches 0; Indels 14; Gaps 3;	431	XX
Qy	72 LAMDTLPDNTRVYEDDNHSSYYVSRVLYGPSEPHSRELWVDVAEANSQVKHTILSNTNHRQ	131	XX
Db	1 LAMDTLPDNTRVYEDDNHSSYYVSRVLYGPSEPHSRELWVDVAEANSQVKHTILSNTNHRQ	60	XX
Qy	132 ASRVTLSPFDFPFYCHPLRQITIATGPIFMGDVTHRMLTATQYAPLAMNFPGYSDNST	191	XX
Db	61 ASRVTLSPFDFPFYCHPLRQITIATGPIFMGDVTHRMLTATQYAPLAMNFPGYSDNST	120	XX
Qy	192 VVYFDNGTGVVVQMDHIVLQGWEKDGSFTFQAAUHHDRIVFAKEIPMSVPEISSQHP	251	XX
Db	121 VVYFDNGTGVVVQMDHIVLQGWEKDGSFTFQAAUHHDRIVFAKEIPMSVPEISSQHP	180	XX
Qy	252 VKTGGLSDAFTNPSPDVPSRRSISFYTRIELDPSKTVTSMSAVEFTPLPTCLQHRSQCD	311	XX
Db	181 VKTGGLSDAFTNPSPDVPSRRSISFYTRIELDPSKTVTSMSAVEFTPLPTCLQHRSQCD	240	XX
Qy	312 ACMSSDLTENCSWCHVLQRQSSGFDYRQEW-MDYGCAQAEGRMCEDQD-----ED	363	XX
Db	241 ACMSSDLTENCSWCHVLQRQSSGFDYRQEW-MDYGCAQAEGRMCEDQD-----ED	294	XX
Qy	364 HDSASPDTSSSPYGDLTSSFLDSLTEDDTKLNPVAGGDLQNLNSPKTKGTGTPH	423	XX
Db	295 TTSASPDTSSSPYGDLTSSFLDSLTEDDTKLNPVAGGDLQNLNSPKTKGTGTPH	354	XX
Qy	424 LGTIVGIVLVVAVIILLAGIYINGHPTSNAAFFIERRPHWPMKFRSHPDHSTYAB	483	XX
Db	355 LGTIVGIVLVVAVIILLAGIYINGHPTSNAAFFIERRPHWPMKFRSHPDHSTYAB	414	XX
Qy	484 VEPSGEKEKGFMEEAQC 500	431	XX
Db	415 VEPSGEKEKGFMEEAQC 431	431	XX

Search completed: November 3, 2005, 20:48:47
Job time : 169 sec(s)

Example 4: Fig 2: 98pp; English.
 XX New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis, graft-versus-host disease, cancers, Alzheimer's disease, Huntington's disease.
 XX The invention relates to a new isolated polypeptide, which has stem cell growth factor-like activity. The new polypeptide, the polynucleotide encoding this polypeptide, or the agonist of the polypeptide are useful for treating a subject in need of enhanced activity or expression of stem cell growth factor-like polypeptide. The antagonist of the polypeptide or

PI Nishikawa M., Labat I., Drmanac RT, Tang YT, Chao C;

XX WPI: 2003-456302/43.

XX PT New stem cell growth factor-like polypeptides and polynucleotides, useful

PT for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis, graft-versus-host disease, cancers, Alzheimer's disease, Huntington's disease.

XX PS Example 4: Fig 2: 98pp; English.

XX The invention relates to a new isolated polypeptide, which has stem cell

CC growth factor-like activity. The new polypeptide, the polynucleotide encoding this polypeptide, or the agonist of the polypeptide are useful CC for treating a subject in need of enhanced activity or expression of stem CC cell growth factor-like polypeptide. The antagonist of the polypeptide or

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 3, 2005, 20:46:00 ; Search time 168 Seconds
 (without alignments)

1245.266 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELMLLVLVREARALSL..... YAEVPSGHKEKGPMEAQCG 500

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 1867879 seqs, 410409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubcaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubcaa/US05_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubcaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubcaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubcaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubcaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubcaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubcaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubcaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubcaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubcaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubcaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubcaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubcaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubcaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubcaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubcaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubcaa/US10F_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubcaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubcaa/US11B_PUBCOMB.pep:*

21: /cgn2_6/ptodata/1/pubcaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/1/pubcaa/US60_PUBCOMB.pep:*

RESULT 1

; Sequence 230, Application US/09918715

; Publication No US20030017157A1

; GENERAL INFORMATION:

; APPLICANT: Brad St. Croix

; APPLICANT: Bert Vogelstein

; APPLICANT: Kenneth Kinzler

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

; FILE REFERENCE: 1107_00134

; CURRENT APPLICATION NUMBER: US/09/918,715

; CURRENT FILING DATE: 2001-08-01

; PRIOR APPLICATION NUMBER: 60/222,599

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: 60/224,360

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/282,850

; PRIOR FILING DATE: 2000-04-11

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: Fast-SEQ for Windows Version 3.0

; SEQ ID NO 230

; LENGTH: 500

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-918-715-230

Query Match Score 100.0%; Score 2691; DB 10; Length 500;

Best Local Similarity 100.0%; Pred. No. 8; 3e-29; Mismatches 0; Indels 0; Gaps 0;

Matches 500; Conservative 0; Gaps 0;

Query 1 MRGELMLLVLVREARALSLPQFGWAKGTVRWNRRARESPGHVSEPR 60

DB 1 MRGELMLLVLVREARALSLPQFGWAKGTVRWNRRARESPGHVSEPR 60

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	2691	100.0	500	10	US-09-918-715-230	Sequence 230, App
2	2691	100.0	500	15	US-10-435-696-79	Sequence 79, App
3	2691	100.0	500	16	US-10-474-794-230	Sequence 230, App
4	2691	100.0	500	16	US-10-357-819-2	Sequence 2, App
5	2691	100.0	500	18	US-10-979-159-230	Sequence 230, App
6	2691	100.0	1002	10	US-09-918-715-179	Sequence 179, App
7	2691	100.0	1002	16	US-10-474-794-179	Sequence 179, App
8	2691	100.0	1002	18	US-10-979-159-179	Sequence 179, App
9	2692	96.7	488	16	US-10-357-819-4	Sequence 4, App
10	2566	95.4	502	14	US-10-154-487-5	Sequence 5, App
11	2209	82.1	500	10	US-09-918-715-192	Sequence 192, App
12	2209	82.1	500	14	US-10-156-487A-6	Sequence 297, App
13	2209	82.1	500	16	US-10-474-794-192	Sequence 297, App
14	2209	82.1	500	16	US-10-474-794-297	Sequence 297, App
15	2209	82.1	500	18	US-10-979-159-297	Sequence 297, App
16	2209	82.1	500	18	US-10-979-159-297	Sequence 297, App
17	2209	82.1	431	10	US-09-912-935-6	Sequence 36, App
18	2185	81.2	431	10	US-10-165-365-6	Sequence 36, App
19	2185	81.2	499	10	US-09-912-935-31	Sequence 31, App
20	1295	48.1	499	15	US-10-168-365-31	Sequence 31, App
21	1295	48.1	529	10	US-09-918-715-189	Sequence 200, App
22	1295	48.1	529	10	US-09-918-715-200	Sequence 28, App
23	1295	48.1	529	10	US-09-912-915-28	Sequence 40, App
24	1295	48.1	529	13	US-10-156-487A-4	Sequence 4, App
25	1295	48.1	529	14	US-10-156-487A-4	Sequence 28, App
26	1295	48.1	529	15	US-10-188-365-31	Sequence 28, App
27	1295	48.1	529	16	US-10-474-794-189	Sequence 200, App
28	1295	48.1	529	16	US-10-474-794-200	Sequence 189, App
29	1295	48.1	529	18	US-10-979-159-189	Sequence 200, App
30	1295	48.1	529	18	US-10-979-159-200	Sequence 200, App
31	1295	48.1	529	18	US-10-979-159-200	Sequence 200, App
32	1294	48.1	529	13	US-10-052-586-772	Sequence 472, App
33	1294	48.1	529	13	US-10-056-500-128	Sequence 472, App
34	1294	48.1	529	14	US-10-174-590-472	Sequence 472, App
35	1294	48.1	529	14	US-10-176-758-772	Sequence 472, App
36	1294	48.1	529	14	US-10-175-737-772	Sequence 472, App
37	1294	48.1	529	14	US-10-174-581-472	Sequence 472, App
38	1294	48.1	529	14	US-10-176-483-772	Sequence 472, App
39	1294	48.1	529	14	US-10-176-749-472	Sequence 472, App
40	1294	48.1	529	14	US-10-176-914-772	Sequence 472, App
41	1294	48.1	529	14	US-10-176-915-772	Sequence 472, App
42	1294	48.1	529	14	US-10-173-705-772	Sequence 472, App
43	1294	48.1	529	14	US-10-175-738-772	Sequence 472, App
44	1294	48.1	529	14	US-10-175-752-772	Sequence 472, App
45	1294	48.1	529	14	US-10-176-482-472	Sequence 472, App

ALIGNMENTS

Qy	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Qy	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGQMEDKGSTFOAHLHHDCRIVFAYKEIPM 240
Db	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Db	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGQMEDKGSTFOAHLHHDCRIVFAYKEIPM 240
Qy	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGP; FMGDVTHRMUTATQVAPMA 180	Qy	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300
Db	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGP; FMGDVTHRMUTATQVAPMA 180	Db	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300
Qy	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGWEKDKGSTFOAHLHHDCRIVFAYKEIPM 240	Qy	301 LPTCLQHRSQDCAACMSDLTFNCSCWCHVILQCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
Db	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGWEKDKGSTFOAHLHHDCRIVFAYKEIPM 240	Db	301 LPTCLQHRSQDCAACMSDLTFNCSCWCHVILQCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
Qy	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300	Qy	361 DEHDHASPDTSFSPPYDGLITSSSLFDLSLTBDPCLNPYAGGDLQONNLSPKTKG 420
Db	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300	Db	361 DEHDHASPDTSFSPPYDGLITSSSLFDLSLTBDPCLNPYAGGDLQONNLSPKTKG 420
Qy	301 LPTCLQHRSQDCAACMSDLTFNCSCWCHVILQCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360	Qy	421 PVHLGTTIVGIVLAVLVAAILAGIYINGHPTSNALPFIERPHWPAMKFRSHPDHST 480
Db	301 LPTCLQHRSQDCAACMSDLTFNCSCWCHVILQCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360	Db	421 PVHLGTTIVGIVLAVLVAAILAGIYINGHPTSNALPFIERPHWPAMKFRSHPDHST 480
Qy	361 DEHDHASPDTSFSPPYDGLITSSSLFDLSLTBDPCLNPYAGGDLQONNLSPKTKG 420	Qy	481 YAEPVPSGHKEGFMBAEQC 500
Db	361 DEHDHASPDTSFSPPYDGLITSSSLFDLSLTBDPCLNPYAGGDLQONNLSPKTKG 420	Db	481 YAEPVPSGHKEGFMBAEQC 500
Qy	421 PVHLGTTIVGIVLAVLVAAILAGIYINGHPTSNALPFIERPHWPAMKFRSHPDHST 480	RESULT 3	US-10-474-794-230
Db	421 PVHLGTTIVGIVLAVLVAAILAGIYINGHPTSNALPFIERPHWPAMKFRSHPDHST 480		; Sequence 230, Application US/10474794
Qy	481 YAEPVPSGHKEGFMBAEQC 500		; Publication No. US20040211793A1
Db	481 YAEPVPSGHKEGFMBAEQC 500		; GENERAL INFORMATION:
			; APPLICANT: Carson-Walter, Eleanor
			; ADDRESS: St. Croix, Brad
			; APPLICANT: Vogelstein, Bert
			; APPLICANT: Kinsler, Kenneth
			; TITLE OF INVENTION: ENDOTHELIAL CBLN EXPRESSION PATTERNS
			; CURRENT APPLICATION NUMBER: US/10/474,794
			; CURRENT FILING DATE: 2003-10-14
			; PRIOR APPLICATION NUMBER: 60/282,850
			; PRIOR FILING DATE: 2001-04-11
			; PRIOR APPLICATION NUMBER: 60/308,829
			; PRIOR FILING DATE: 2001-08-01
			; NUMBER OF SEQ ID NO: 359
			; SOFTWARE: FastSEQ for Windows Version 4.0
			; SEQ ID NO: 230
			; LENGTH: 500
			; TYPE: PRT
			; ORGANISM: Homo sapiens
			US-10-474-794-230
Qy	1 MRGEIWLVLVLRAREARALSPOPGHDEGPGSWAAKTVGRNNRARESPGHVSEPR 60	Query Match	100.0%; Score 2691; DB 16; Length 500;
Db	1 MRGEIWLVLVLRAREARALSPOPGHDEGPGSWAAKTVGRNNRARESPGHVSEPR 60	Best Local Similarity	100.0%; Pred. No. 8_3e-249; Mismatches 0; Indels 0; Gaps 0;
Qy	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Qy	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120
Db	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Db	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120
Qy	1 MRGEIWLVLVLRAREARALSPOPGHDEGPGSWAAKTVGRNNRARESPGHVSEPR 60	Qy	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGF; FMGDVTHRMUTATQVAPMA 180
Db	1 MRGEIWLVLVLRAREARALSPOPGHDEGPGSWAAKTVGRNNRARESPGHVSEPR 60	Db	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGF; FMGDVTHRMUTATQVAPMA 180
Qy	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Qy	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGWDKGSTFOAHLHHDCRIVFAYKEIPM 240
Db	61 TQLSODLGCGTILAMDTLPDRTRVVEDNHSYYVSRLYGPSEPHSRELWVAEANRSQK 120	Db	181 NFNPGYSDNSTVVYFDNGTVFVWMDHVLQGWDKGSTFOAHLHHDCRIVFAYKEIPM 240
Qy	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGF; FMGDVTHRMUTATQVAPMA 180	Qy	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300
Db	121 IHTLISNTHQASRVVLSPDFPPYCHPLQQTIAATGGF; FMGDVTHRMUTATQVAPMA 180	Db	241 SVPEISSOHPVKTGSDAFMLNPSPDVPESSRSIFFYHRIELDPSKVTSMSAVEFTP 300

RESULT 4
US-10-357-819-2

Sequence 2, Application US-10337819
Publication No. US20040259774A1

GENERAL INFORMATION:

APPLICANT: Alvarez, Enrique
EDINGER, Shlomit R.
Gangoli, Esha A.
Gerlach, Valerie L.
Gorman, Linda
Guo, Xiaojia
Ji, Weichen
Ketkuda, Ramesh
Li, Li
Miller, Charles E.
Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
Rieger, Daniel K.
Shanoy, Suresh A.
Shimkets, Richard A.
Spytrek, Kimberly P.
Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21442-538A

CURRENT APPLICATION NUMBER: US-10/357,819
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 10/085,198
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/353,301
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 60/355,099
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/356,424
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/358,239
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/358,608
NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraseQList version 0.1
SEQ ID NO 2
LENGTH: 500
TYPE: PRT
ORGANISM: Homo sapiens

RESULT 5
US-10-979-159-230

Sequence 230, Application US-10979159
Publication No. US20050142138A1

GENERAL INFORMATION:

APPLICANT: Brad St. Croix
EDINGER, Bert Vogelstein
GANGOLI, Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107-00134
CURRENT APPLICATION NUMBER: US-10/979,159
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US-09/918,715
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 230
LENGTH: 500
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 100.0%; Score 2691; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 8..3e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MREGLWLLVILVREARALSLPSQPGAGHDEPGGCGWAAGKTVGRNMRARESPGHVSEPR 60
Db 1 MREGLWLLVILVREARALSLPSQPGAGHDEPGGCGWAAGKTVGRNMRARESPGHVSEPR 60

Qy 61 TQLSQDGGTTLAMDLPDNTRVVEDNHSYYSYSLXGPSEPHSRELWDVAEANSQVK 120
Db 61 TQLSQDGGTTLAMDLPDNTRVVEDNHSYYSYSLXGPSEPHSRELWDVAEANSQVK 120

Qy 121 IHTLISNTHROASRVLSDFDPFGHPLRQITATGGIFMGDVITHRMLTATQVAPLMA 180
Db 121 IHTLISNTHROASRVLSDFDPFGHPLRQITATGGIFMGDVITHRMLTATQVAPLMA 180

Qy 181 NENPGYSDNSTVYFVDNGTYFVQMDHYLOGMEDKGSSFTFOALHHDRIVPAYKEIPM 240
Db 181 NENPGYSDNSTVYFVDNGTYFVQMDHYLOGMEDKGSSFTFOALHHDRIVPAYKEIPM 240

Qy 241 SVBPISSSOHPVKTGSLDAFMILNPSPDVPESSRRSFIFYHRTLDPSKVTSMSAVEFTP 300
Db 241 SVBPISSSOHPVKTGSLDAFMILNPSPDVPESSRRSFIFYHRTLDPSKVTSMSAVEFTP 300

Qy 301 LPFCLOQRHRSQDACMSDLTENCSWCHVTLQRCSSGFDRYQEMMDYGCQAEGRMCEDFQ 360
Db 301 LPTCLOQRHRSQDACMSDLTENCSWCHVTLQRCSSGFDRYQEMMDYGCQAEGRMCEDFQ 360

Qy 361 DEDHDSASPDTSFSPYDSDLTTSSLFSDLSLTEDDTKLNPAGGDLQNNLSPKTGT 420
Db 361 DEDHDSASPDTSFSPYDSDLTTSSLFSDLSLTEDDTKLNPAGGDLQNNLSPKTGT 420

Qy 421 PVHLGTTIVLVAIILAGIYINGHPTSNALFPIERPHWPAMKFRSHPDHST 480
Db 421 PVHLGTTIVLVAIILAGIYINGHPTSNALFPIERPHWPAMKFRSHPDHST 480

Qy 481 YAEVPSGHEKEGFMMEAQC 500
Db 481 YAEVPSGHEKEGFMMEAQC 500

181 NFPQYSIDNSTVYYFDNGTVFVVQMDHYYLQGNEDKGSFTPQAALHHDRIVPAYKEIPM 240
 Qy 683 NFPQYSIDSTVYYFDNGTVFVVQMDHYYLQGNEDKGSFTPQAALHHDRIVPAYKEIPM 742
 Db 741 SVPETISSQHPVKTGGLSDAFMLINPSDVPESRRSIFFYHRIELDPSKVTMSAVENTP 300
 Qy 742 SVPETISSQHPVKTGGLSDAFMLINPSDVPESRRSIFFYHRIELDPSKVTMSAVENTP 802
 Db 743 SVPETISSQHPVKTGGLSDAFMLINPSDVPESRRSIFFYHRIELDPSKVTMSAVENTP 860
 Qy 301 LPTCLQHRCDACMSDLTFCNSWCHVLQRCSGGPDRYRQEWMDYGCQAQAEGRMCEDFQ 420
 Db 803 LPTCLQHRCDACMSDLTFCNSWCHVLQRCSGGPDRYRQEWMDYGCQAQAEGRMCEDFQ 862
 Qy 361 DEHDASASDPTSPSPYDGLTTSSLFDSLTDYKLNPYAGDGLQNNLSPKTGT 420
 Db 863 DEHDASASDPTSPSPYDGLTTSSLFDSLTDYKLNPYAGDGLQNNLSPKTGT 922
 Qy 361 DEHDASASDPTSPSPYDGLTTSSLFDSLTDYKLNPYAGDGLQNNLSPKTGT 480
 Db 863 DEHDASASDPTSPSPYDGLTTSSLFDSLTDYKLNPYAGDGLQNNLSPKTGT 982
 Qy 421 PVHLGTTIVLAVLVAIILAGIYINGHTPSNALFFIERPHWPAMKFRSHPDHST 480
 Db 923 PVHLGTTIVLAVLVAIILAGIYINGHTPSNALFFIERPHWPAMKFRSHPDHST 982
 Qy 481 YAEVPSGHEKEGMMEAQC 500
 Db 983 YAEVPSGHEKEGMMEAQC 1002

RESULT 9
 US-10-357-819-4
 Sequence 4, Application US/10357819
 ; GENERAL INFORMATION:
 ; Publication No. US2004025974A1
 ; APPLICANT: Alvarez, Enrique
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gangoli, Baha A.
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Li, Li
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-518A
 ; CURRENT APPLICATION NUMBER: US/10/357,819
 ; CURRENT FILING DATE: 2003-02-03
 ; PRIOR APPLICATION NUMBER: 09/584,411
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 09/584,411
 ; PRIOR FILING DATE: 2003-02-14
 ; PRIOR APPLICATION NUMBER: 09/783,436
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: 09/353,301
 ; PRIOR FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: 60/355,099
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: 60/356,424
 ; PRIOR FILING DATE: 2002-02-12
 ; PRIOR APPLICATION NUMBER: 60/358,239
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: 60/358,608
 ; PRIOR APPLICATION NUMBER: 60/359,367
 ; PRIOR FILING DATE: 2002-02-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; SOFTWARE: Curaseqist version 0.1
 ; SEQ ID NO 4

RESULT 8
 US-10-979-156-179
 Sequence 179, Application US/10979159
 ; GENERAL INFORMATION:
 ; Publication No. US20050142138A1
 ; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Voelstein
 ; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107-00134
 ; CURRENT APPLICATION NUMBER: US/10/979,159
 ; CURRENT FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US/09/918,715
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/222,599
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/224,360
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 179
 ; LENGTH: 1002
 ; TYPE: PRTR
 ; ORGANISM: Homo sapiens
 US-10-979-159-179

Query Match 100.0%; Score 2691; DB 18; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 2, 5e-28;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGEFLWLLVLRREAARALSPQGAGHDEPGSGWAANGTVCRWNRARESPOHVSEPR 60
 Db 503 MRGEFLWLLVLRREAARALSPQGAGHDEPGSGWAANGTVCRWNRARESPOHVSEPR 562
 Qy 61 TQLSQDLSGGTLANDTLPNRTRVVEDNHYYVSRLYGPSEPHISRELWVDAEANRSQV 120
 Db 563 TQLSQDLSGGTLANDTLPNRTRVVEDNHYYVSRLYGPSEPHISRELWVDAEANRSQV 622
 Qy 121 IHTLNSNTHROASRVLSFDFPFYGHPLQTATGGTFMGDVYTHMLTATQYVAPIMA 180
 Db 623 IHTLNSNTHROASRVLSFDFPFYGHPLQTATGGTFMGDVYTHMLTATQYVAPIMA 682
 Qy 181 NFPQYSIDNSTVYYFDNGTVFVVQMDHYYLQGNEDKGSFTPQAALHHDRIVPAYKEIPM 240
 Db 683 NFPQYSIDNSTVYYFDNGTVFVVQMDHYYLQGNEDKGSFTPQAALHHDRIVPAYKEIPM 742

```

/
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-819-4

Query Match          96 7%; Score 2602; DB 16; Length 488;
Best Local Similarity 97 4%; Pred. No. 2.8e-240;
Matches 487; Conservative 1; Mismatches 0; Indels 12; Gaps 1;

Qy      1 MRGEIWLWVILVREARALSPQPGCHDEPGSGWAAGKTYGRMNMRARRSPGHYSEPRD 60
Db      1 MRGEIWLWVILVREARALSPQPGCHDEPGSGWAAGKTYGRMNMRARRSPGHYSEPRD 60
Db      1 TQLSDLGCGTTLAMPDLPDTRTRVYEDNHSSYYSLGPSEPHSRELWDVAEARSQVK 120
Qy      61 TQLSDLGCGTTLAMPDLPDTRTRVYEDNHSSYYSLGPSEPHSRELWDVAEARSQVK 120
Db      61 TQLSDLGCGTTLAMPDLPDTRTRVYEDNHSSYYSLGPSEPHSRELWDVAEARSQVK 120
Qy      121 IHTLISNTHQASRVLSPDPEPYCHPLRQITIATCGF1IMGDVTHRLMTATOYAPLMA 180
Db      121 IHTLISNTHQASRVLSPDPEPYCHPLRQITIATCGF1IMGDVTHRLMTATOYAPLMA 180
Qy      181 NFPQYSDNSTYYFDNGTIVFVQDHDVYLQWDEBKGSFTFOAALHHDGR1IVFAVKBIPM 240
Db      181 NFPQYSDNSTYYFDNGTIVFVQDHDVYLQWDEBKGSFTFOAALHHDGR1IVFAVKBIPM 240
Qy      241 SVPETISSOHPVKTGCLSDAFMLNPSDVPESRRSIFETHRIELDPSKTVTMSMSAVEFTP 300
Db      241 SVPETISSOHPVKTGCLSDAFMLNPSDVPESRRSIFETHRIELDPSKTVTMSMSAVEFTP 300
Qy      301 LPTC1QHRSQDCAMSSD1T1FNCWSKTVLQPCSSGDRYQEWMDIGCAQAEGRMCEDFQ 360
Db      301 LPTC1QHRSQDCAMSSD1T1FNCWSKTVLQPCSSGDRYQEWMDIGCAQAEGRMCEDFQ 360
Qy      361 DEDHMASPDTSFSYDGD1TTSSFLIDSLLTDDTKLNPYAGGDGLONNLSPPTKGT 420
Db      361 DEDHMASPDTSFSYDGD1TTSSFLIDSLLTDDTKLNPYAGGDGLONNLSPPTKGT 420
Qy      421 PVHLTGIVLVALVAVAILLAGTYINGHPTSNAAFFTERRPHWPAWKFRSHIDPHST 480
Db      409 PVHLTGIVLVALVAVAILLAGTYINGHPTSNAAFFTERRPHWPAWKFRSHIDPHST 468
Qy      481 YAEVEPSGHAKREGMNEAQ 500
Db      469 YAEVEPSGHAKREGMNEAQ 488

RESULT 10
US-10-156-487A-5
; sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliver, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/283,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match          95 4%; Score 2566; DB 14; Length 502;
Best Local Similarity 95 9%; Pred. No. 8.3e-237;
Matches 487; Conservative 0; Mismatches 7; Indels 14; Gaps 3;
Qy      1 MRGEIWLWVILVILVREARALSPQPGCHDEPGSGWAAGKTYGRMNMRARRSPGHYSEPRD 60

```

Qy	120 KIHTILSNTHROASRVLSPDFPFYGHPLRQITIATGGTIFMGDVIRHMLTATOYAPLM 179	Db	181 ANFNPGYSDNSTAYFDNGTVFVQWDAYLQDREDRGSPTFOALHGRIVFGYKEIP 240
Db	121 KIHLSSSHROASRVLSPDFPFYGHPLRQITIATGGTIFMGDMHLRMLTATOYAPLM 180	Qy	240 MSVPBISQQHPVKTGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 299
Qy	180 ANFNPGYSDNSTVYYFDNGTVFVQWDHYTQLQGMDKGSEFTFOALHHGRIVFAKEIP 239	Db	241 MAVLDISSAQHPVKAGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 300
Db	181 ANFNPGYSDNSTVAYFDNGTVFVQWDHYTQLQDREDRGSPTFOALHGRIVFGYKEIP 240	Qy	300 PLPFLQRHSRSCDAFMISDLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 359
Qy	240 MSVPBISQQHPVKTGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 299	Db	301 PLPFLQHQSCDTCVSSNLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 360
Db	241 MAVLDISSAQHPVKAGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 300	Qy	360 QDEHDSSASPDTSFSPYGDPLTTSSLFDISLTEDDTKLNPYAGGDSLQNNLSPKTKG 419
Qy	300 PLPFLQRHSRSCDAFMISDLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 359	Db	361 QDDSHYSASPDSSSPFPNGD-STSSSLFDISLTEDDTKLNPYAGGDSLQNNLSPKTKG 419
Db	301 PLPFLQHQSCDTCVSSNLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 360	Qy	420 TPVHLGTIVGIVLAVLVAIILAGIYINGHPTSNAAFFIERPHWPAKFPSPHDHS 479
Qy	360 QDEHDSSASPDTSFSPYGDPLTTSSLFDISLTEDDTKLNPYAGGDSLQNNLSPKTKG 419	Db	420 PPVHLGTIVGIVLAVLVAIILAGIYISGHPNNSNAAFFIERPHWPAKFPHNPHNS 479
Db	361 QDDSHYSASPDSSSPFPNGD-STSSSLFDISLTEDDTKLNPYAGGDSLQNNLSPKTKG 419	Qy	480 TYAEPSPSHEKEGMEAEQC 500
Qy	420 TPVHLGTIVGIVLAVLVAIILAGIYINGHPTSNAAFFIERPHWPAKFPSPHDHS 479	Db	480 TYAEPSPSHEKEGMEAEQC 500
Db	420 PPVHLGTIVGIVLAVLVAIILAGIYISGHPNNSNAAFFIERPHWPAKFPHNPHNS 479	RESULT 13	
Qy	480 TYAEPSPSHEKEGMEAEQC 500	; Sequence 6, Application US/10156487A	
Db	480 TYAEPSPSHEKEGMEAEQC 500	; Publication No. US20030092025A1	
; GENERAL INFORMATION:			
;	APPLICANT: Brad St. Croix	;	GENERAL INFORMATION:
;	APPLICANT: Bert Voelztein	;	APPLICANT: Juan, Todd
;	APPLICANT: Kenneth Kinzler	;	APPLICANT: Oliner, John
;	TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS	;	TITLE OF INVENTION: Endothelial Marker 7a Molecules and Uses Thereof
;	FILE REFERENCE: 1107_00134	;	FILE REFERENCE: 01-072-A
;	CURRENT APPLICATION NUMBER: US/09/918,715	;	CURRENT APPLICATION NUMBER: US/10/156,487A
;	PRIOR APPLICATION NUMBER: 2001-08-01	;	CURRENT FILING DATE: 2002-09-10
;	PRIOR FILING DATE: 2000-08-02	;	PRIOR APPLICATION NUMBER: 60/293,852
;	PRIOR APPLICATION NUMBER: 60/222,599	;	PRIOR FILING DATE: 2001-05-25
;	PRIOR FILING DATE: 2000-08-02	;	NUMBER OF SEQ ID NOS: 15
;	PRIOR APPLICATION NUMBER: 60/224,360	;	SOFTWARE: PatentIn Ver. 2.0
;	PRIOR FILING DATE: 2000-08-11	;	SEQ ID NO 6
;	PRIOR APPLICATION NUMBER: 60/282,850	;	LENGTH: 500
;	PRIOR FILING DATE: 2000-04-11	;	TYPE: PRT
;	NUMBER OF SEQ ID NOS: 358	;	ORGANISM: Mus musculus
;	SOFTWARE: FirstSeq For Windows Version 3.0	;	US-10-156-487A-6
;	SEQ ID NO 297	;	Query Match 82.1%; Score 2209; DB 10; Length 500;
;	LENGTH: 500	;	Best Local Similarity 81.6%; Pred. No. 1.5e-203; Indels 2; Gaps 2;
;	ORGANISM: Mouse	;	Matches 46; Mismatches 44; Gaps 2;
;	US-09-918-715-297	;	1 MRGELWLL-VLVIREAARALSPQPGAHDEGPMSGWAAGKTYRGWNRARESPGHVSEPD 59
;	Query Match 82.1%; Score 2209; DB 10; Length 500;	;	1 MRAQWLQLLLRGARALSPATPAGNEQGDSAWTKRTQWSRPRESPAQLKFG 60
;	Best Local Similarity 81.6%; Pred. No. 1.5e-203; Indels 2; Gaps 2;	;	1 RTQLSQDQGGTLAMDTLPDNTRTRVVEDNHSYVSRLYGPSPHSEPSRELWVDVANEANRSOV 119
;	Matches 46; Mismatches 44; Gaps 2;	;	1 RTQLSQDQGGSLAIDTLPDNTRTRVEDNHNTYVSRVGPGEKRSQDLMWVDAVANSHV 120
;	1 MRGELWLL-VLVIREAARALSPQPGAHDEGPMSGWAAGKTYRGWNRARESPGHVSEPD 59	;	120 KIHTILSNTHROASRVLSPDFPFYGHPLRQITIATGGTIFMGDVIRHMLTATOYAPLM 179
;	1 MRAQWLQLLLRGARALSPATPAGNEQGDSAWTKRTQWSRPRESPAQLKFG 60	;	121 KIHLSSSHROASRVLSPDFPFYGHPLRQITIATGGTIFMGDMHLRMLTATOYAPLM 180
;	Qy	;	180 ANFNPGYSDNSTAYFDNGTVFVQWDAYLQDREDRGSFTFOALHGRIVFGYKEIP 240
;	Db	;	181 ANFNPGYSDNSTAYFDNGTVFVQWDAYLQDREDRGSFTFOALHGRIVFGYKEIP 240
;	Qy	;	240 MSVPBISQQHPVKTGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 299
;	Db	;	241 MAVLDISSAQHPVKAGLSDAFMILNPSDPVPESSRRSIFEYRIELDPSKVTMSAVFT 300
;	Qy	;	300 PLPFLQRHSRSCDAFMISDLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 359
;	Db	;	301 PLPFLQHQSCDTCVSSNLTFCNSWCHMQLQCSGGFDRQEWMDYGAQEAEGRMCDF 360
;	Qy	;	180 ANFNPGYSDNSTVYYFDNGTVFVQWDHYTQLQGMDKGSEFTFOALHHGRIVFAKEIP 239

360 QDEDHDSASBDTSSPSPYDGLTTSSSLFDSLTDPTKLNPYAGGDCQLQNNLSPKTKG 419
 Qy 361 QDDSHYSASDSSPFDNCD-STTSSSLFDSLTDPTKLNPYAGGDLPDHSSPKSG 419
 Db 362 TPVHLGTTIVGIVLAVLVAAILLAGIYINGHTPSNAALFFIERPHWPAKFRSHPDHS 479
 Qy 363 TPVHLGTTIVGIVLAVLVAAILLAGIYINGHTPSNAALFFIERPHWPAKFRSHPDHS 479
 Db 364 TPVHLGTTIVGIVLAVLVAAILLAGIYISGHPNNSNAALFFIERPHWPAKFRSHPDHS 479
 Result 15
 US-10-474-794-297
 ; Sequence 297, Application US/10474794
 ; Publication No. US20040213793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carson-Walter, Eleanor
 ; APPLICANT: St. Croix, Brad
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107.00119
 ; CURRENT APPLICATION NUMBER: US/10/474,794
 ; CURRENT FILING DATE: 2003-10-14
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 60/308,829
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 359
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 297
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-10-474-794-297

Query Match 82.1%; Score: 2209; DB: 16; Length: 500;
 Best Local Similarity: 81.6%; Pred. No. 1.5e-202;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGEWLIL-VLVLRAARALSPQGAGHDGPSSGWAAKCTVRGWNRARESPGHVSEPD 59
 Db 1 MRAQWLQDILLRQARALSPATPGHNEQGDSAWTAETTRQSSRRPESPAQVLRKG 60
 Qy 2 MRGEWLIL-VLVLRAARALSPQGAGHDGPSSGWAAKCTVRGWNRARESPGHVSEPD 59
 Db 2 RTOLSDQDUGGTLMNDLDPNRTTRVVEDDNHSSYYTSRLYGPSEPHSRRELWDVAANRSQV 119
 Qy 3 MRGEWLIL-VLVLRAARALSPQGAGHDGPSSGWAAKCTVRGWNRARESPGHVSEPD 59
 Db 3 KTOQSDQDGGSLAIDTLDPNRTTRVVEDDNHNTYTSRVGPGEKSQDLWDLAVANRSHV 120
 Qy 4 MRGEWLIL-VLVLRAARALSPQGAGHDGPSSGWAAKCTVRGWNRARESPGHVSEPD 59
 Db 4 MRAQWLQDILLRQARALSPATPGHNEQGDSAWTAETTRQSSRRPESPAQVLRKG 60
 Query Match 82.1%; Score: 2209; DB: 16; Length: 500;
 Best Local Similarity: 81.6%; Pred. No. 1.5e-202;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 5 MRGEWLIL-VLVLRAARALSPQGAGHDGPSSGWAAKCTVRGWNRARESPGHVSEPD 59
 Db 5 KTOQSDQDGGSLAIDTLDPNRTTRVVEDDNHNTYTSRVGPGEKSQDLWDLAVANRSHV 120
 Qy 6 RTOLSDQDUGGTLMNDLDPNRTTRVVEDDNHSSYYTSRLYGPSEPHSRRELWDVAANRSQV 119
 Db 6 KTOQSDQDGGSLAIDTLDPNRTTRVVEDDNHNTYTSRVGPGEKSQDLWDLAVANRSHV 120
 Qy 7 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 7 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 8 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 8 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 9 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 9 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 10 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 10 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 11 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 11 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 12 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 12 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 13 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 13 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 14 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 14 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 15 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 15 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 16 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 16 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 17 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 17 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 18 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 18 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 19 ANFNGYSNDSTVYTFDNGTVFVWQDHYLOGMDKGSFTFOQALHHDRGIVSAYKEIP 179
 Db 19 KHRLLSSHQASRVLISDFPFGHPLRQITATGGFIFMGDMHLRMLTATQVAPLM 180
 Qy 20 MSVPETSSQHPVKTGLSDAFMILNPSPDPSRRSIPEYHRIELDPSKVTSMSAVEFT 299
 Db 20 PLPTCLQHQSCDTCVSSNLTFCNSMCHVLRQCSSSFDRYQEMNYGCQAEGRMCEIP 359
 Qy 21 MSVPETSSQHPVKTGLSDAFMILNPSPDPSRRSIPEYHRIELDPSKVTSMSAVEFT 299
 Db 21 PLPTCLQHQSCDTCVSSNLTFCNSMCHVLRQCSSSFDRYQEMNYGCQAEGRMCEIP 360
 Qy 22 MSVPETSSQHPVKTGLSDAFMILNPSPDPSRRSIPEYHRIELDPSKVTSMSAVEFT 299
 Db 22 PLPTCLQHQSCDTCVSSNLTFCNSMCHVLRQCSSSFDRYQEMNYGCQAEGRMCEIP 360
 Qy 23 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 23 QDDEHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 24 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 24 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 25 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 25 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 26 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 26 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 27 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 27 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 28 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 28 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 29 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 29 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 30 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Db 30 QDEDHDSASPDTSFSPSYDGLTITSSSLFIDLSDLTEDDTKLNPYAGGDLQNNLSPKTKG 419
 Qy 31 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 31 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 32 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 32 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 33 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 33 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 34 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 34 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 35 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 35 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 36 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 36 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 37 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 37 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 38 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 38 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 39 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 39 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 40 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 40 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 41 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 41 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 42 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 42 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 43 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 43 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 44 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 44 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 45 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 45 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 46 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 46 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 47 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 47 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 48 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 48 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 49 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 49 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Qy 50 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479
 Db 50 QDDSYTSSPDSSPFNCED-SITTSPLAEQGDPHSSPKSG 479

Mon Nov 7 09:23:26 2005

usb-09-918-715-230.rapb

Page 9

Search completed: November 3, 2005, 20:54:14
Job time : 170 Secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model
Run on: November 3, 2005 ; Search time 41 Seconds
Title: US-09-918-715-230
Perfect score: 2691
Sequence: 1 MRGELMVLVLVREARALS.....YAEVTPSGHKEKGPMEEAQC 500
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79;*
1: PIR1;*
2: PIR2;*
3: PIR3;*
4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	611	22.7	476	2	T19786		hypothetical protein
2	126	4.7	1161	1	S31213		nitrogen precursor
3	115.5	4.3	1568	2	T09074		semaphorin receptor
4	103.5	3.8	979	2	C86446		probable cellulose
5	101.5	3.8	743	2	T09173		EH domain protein
6	101	3.8	733	2	E86345		hypothetical protein
7	100	3.7	535	2	S18606		phosphoenolpyruvate
8	99	3.7	1133	2	T12529		hypothetical protein
9	98	3.6	345	2	T16074		hypothetical protein
10	98	3.6	1502	2	S45429		probable membrane
11	97	3.6	708	2	I83196		NEDD-4 ORF - mouse
12	96	3.6	397	2	S33415		corticosteroid-bin
13	96.5	3.6	679	2	T19703		hypothetical protein
14	95.5	3.5	399	1	S71480		homoeotic protein H
15	95.5	3.5	887	2	S70642		ubiquitin ligase N
16	95.5	3.5	2120	2	T30243		alpha tectorin - c
17	93	3.5	774	2	JC7265		nephrilysin (BC 3.4
18	93	3.5	979	1	JC2349		protein-tyrosine-p
19	93.5	3.5	996	2	I48721		PTP 35 protein - m
20	93	3.5	1977	2	S54771		sodium channel alp
21	93	3.5	491	2	AG3506		phosphoenolpyruvat
22	93	3.5	1085	2	S55352		IFN1 protein - yeast
23	92.5	3.4	441	2	JC7653		peptidase lyase (EC
24	92	3.4	852	2	A85041		probable receptor
25	91.5	3.4	614	2	A98241		hypothetical protein
26	91.5	3.4	614	2	F86088		hypothetical protein
27	91.5	3.4	810	1	P2WMBB		2A Protein - broad
28	91	3.4	1042	2	A57534		musin 5AC (clone L
29	91	3.4	633	2	S47144		mating type A prot

ALIGNMENTS

RESULT 1	T19786	hypothetical protein C36E8.3 - Caenorhabditis elegans
C;Species:	Caenorhabditis elegans	
C;Date:	15-Oct-1999	#sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession:	T19766	
R;Wilkinson, J.; Barlow, K.		submitted to the EMBL Data Library, August 1994
A;Reference number:	Z19786	
A;Accession:	T19786	
A;Status:	preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA		
A;Residues: 1-476 < WIL>		
A;Cross-references: UNIPROT:Q18500; EMBL:235597; PIDN:CAR84646.1; CBSPDB:GN00021; CBSP: C3		
A;Experimental source: clone C36E8		
C;Genetics:		
A;Map position: 3		
A;Introns: 23/1, 101/3, 152/3; 206/3; 235/1, 255/3; 320/1; 445/2		
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3		
Query Match 22.7%; Score 611; DB 2; Length 476;		
Best Local Similarity 34.2%; Pred. No. 5.6-42; Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;		
Qy 46 RRARESPGHIVSEPDRTQSL-----ODLGCGTLLAMDTLPDNTRVVEDHSYYVSRLYGRS 100		
Db 62 RTARAAP---IPKRSLASEQDEEDIDPATATIP--PDVEVKNDMDHQYYQAEFTFGD 115		
Oy 101 EPHSRLEWYDVAEANSQVKI---HTLISNTNTHROASRVVLSDFFPFYGHPLRQITIATG 156		
Db 116 GETLKTYWINVBOQMRRPKAVGNTSHPLISQSTRAVERAQLQPKFPXGHKMSNLNTIAG 175		
Oy 157 GFIFMGDVTHRMLTATQYAPIMANENPGYSDNSTVYVFDDNGTVFVQDMHXYLQGWEDK 216		
Db 176 GFIYIGDISHNWLAATQTAPLMANFH-YLANSNIVYADDGFLVWEWRVNLQVKEDDE 234		
Oy 217 GSFTFQALHHQDRIVFAKYEKIPMSVPEISSLSSHPVPTGGLSDAFMLIN--PSPDPVPSRR 274		
Db 235 HSFTFTQTLHKNSDIVFYKDYYDIDSNTSDANHPVKLGISDAYMFKEHLHQAVP--K 291		
Oy 275 RSIFYEHRTELDPSKVTSMSAVENTPLPTCLQHRSIDACMSSDIT-FNCWSWCHVL QR--- 330		
Db 292 RVIYEYHRIBIAQKIVSNTVTLKAQPTCISDTCDCNLPFHICLWCAKSHGG 351		
Oy 331 --CS--SGFDRYQEWMDYGCQAEGRMCE-DFODEDHDSAS-PDTTSFSPYDGDLLRTS 384		
Db 352 PFTCTDEAGHRRHQWFGNQYORSKALYCDADDEDEYDDEPQQLMPNEGH--TV 408		
Oy 385 SSELPIDSLTTEDDTKLNPYAGGDGLQNLSPTKGTGIVHLGTVLAVLVAAILNG 444		
Db 409 LPDDADKMKKTDKTTSSESDMEKGHKCKKEPK---GG 442		

QY	445 IYINGHP-TSNAALP	458	A;Accession: T09074 A;Status: preliminary; translated from GB/EMBL/DDJB
Db	443 VATTAHPVTSQAATP	458	A;Molecule type: mRNA A;Cross-references: UNIPROT:Q060486; EMBL:AF030339; NID:9317671; PID: AAC18823.1; PID:9317671
RESULT 2			
S31213	nidogen precursor - sea squirt (<i>Halocynthia roretzii</i>)		A;Experimental source: tissue type foreskin; cell type fibroblast C;Genetics: A;Gene: VESPR
N;Alternate names: entactin			C;Keywords: receptor; signal transduction
C;Species: <i>Halocynthia roretzii</i>			Query Match 4.3%; Score 115.5; DB 2; Length 1568;
C;Accession: S31213	Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004		Best Local Similarity 20.6%; Pred. No. 1; Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.	Bur, J. Bloch, 213, 11, 19, 1993		Qy 39 GTVRGWNRAESPCHVSEEDRT---QISODIAGTLMADTLPDRTRVVENDHYYYS 94
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of cDNA sequences.	A;Reference: S31213; MUID:93238876; PMID:8477887		Db 256 GAATCPMSAR---IAQSTEVLFQGASLDCCGH---PDGR-----R 292
A;Molecule type: mRNA			Qy 95 RLYGPSEPHSRELWVDV-AEANRSQVKIKHTI-----LSNTHRQASRVVLSF-----139
A;Residues: 1-1161 <NAK>			Db 293 LLSSLSLVFALDWGVFSAAGGQERSPTTAQAKRVSDFRMSEQARAKRVSDFRMSDFKTAES 352
A;Cross references: UNIPROT:Q04901; EMBL:D14038; NID:9217363; PID:92173			Qy 140 -----DFFPYGHPLRQQTATGGPIFMGDVIRHMLTATQVAPIMANFPGYSDMSNTVYV 194
C;Superfamily: Ascidian nidogen; EGF homology; LDL receptor YWTD-containing repeat homolog	C;Key words: basement membrane; collagen binding; disulfide bond; duplication; extracellular		Db 353 HCKRGDOPERVQPLAASLU-----IHSPLDTSV-YGTVM-----NRTVLF 391
F;1-20/Domain: signal sequence #status Predicted #SIG>			Qy 195 FDNGTVFVQQWDHFLYLQGWEDKGSFTFQALHHDRGI--VFAYKEIIPNSVPEI--SSSQ 249
F;21-116/Domain: product: nidogen #status Predicted #MAT>			Db 392 LGTG-----DGQLKVILGENLTSCNPETVYIEIKE 422
F;1-306/Domain: EGF homology <EG1>			Qy 250 HPYVTKGLSDAFTINPSPDVPESSRRSFIFYEHRIELDPSKVTSMASVETPLPLCLOHRS 309
F;603-673/Domain: thryoglobulin type I repeat homology <THY1>			Db 423 TPV-----FYKIVPDP-----VNNTYI-----LTGAEVTRIRVANCNHKS 460
F;686-748/Domain: thryoglobulin type I repeat homology <THY2>			Qy 310 CDACMSSDLTENCSWCHVILQRCSGGEDRYRQE---WMDYGCQAQEAEGRMCEDFQ---D 361
F;752-819/Domain: thryoglobulin type I repeat homology <THY3>			Db 461 CSECTA-TDPHCEWCHSHLQRCTFQGDCVHSENLENLWDI----SSGARKCPKIQIIRR 515
F;900-943/Domain: LDL receptor YWTD-containing repeat homology <YW1>			Qy 362 EDHDSASPDTSFSP 375
F;944-986/Domain: LDL receptor YWTD-containing repeat homology <YW2>			Db 516 KEXKTTVTMVGSPSP 529
F;987-1031/Domain: LDL receptor YWTD-containing repeat homology <YW3>			
F;1032-1075/Domain: LDL receptor YWTD-containing repeat homology <YW4>			
F;1076-1114/Domain: LDL receptor YWTD-containing repeat homology <YW5>			
F;1129-1158/Domain: EGF homology <EG2>			
F;1177, 334, 360, 484/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 4.7%; Score 126; DB 1; Length 1161;			
Best Local Similarity 23.5%; Pred. No. 0.094;	Mismatches 34; Indels 86; Gaps 12;		
Matches 64; Conservative			
Qy 137 LSFDPPFYKPLRQQTATGGIFM-----GDIVHHMLTATQVAPLMAN-----181			RESULT 4
Db 47 LSMPDPPFYKPLRQQTATGGIFM-----GDIVHHMLTATQVAPLMAN-----181			C8446 probable cellulose synthase catalytic subunit (imported) - <i>Arabidopsis thaliana</i>
Qy 182 --FNPQGSNDSTVY-----FDNGTVFVQWDHMLQGKSGSFTFOA 224			C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)
Db 98 DIFFREKHNDIATIARNDVYRASFLETDGFENASQVFTWDKVQSASBDGVTFFOI 157			C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Qy 225 LHHGDRIVAA-YKEIPMSVEIS---SSQHQVKTGSDA---FVTLINPSP---DV 269			C;Accession: C8446
Db 158 VATDGAATTAFLYFQDGAVGENAVKGTVNEATARGNNDGGRQELTISADELLGCDDN 217			R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Qy 270 PESRRRSIFEVHRYELDPSKVTMSAVENTPLPLTCQHSSCDACMSSDLTENCSWCHVLUQ 329			Nature 408, 816-820, 2000
Db 218 AGSQGQWIFIGGMFNNENASEKSE---KH-----HVK 249			C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Qy 330 RCSSGFDRYRQEW-MDYGCAQEA-GRMCEDF 359			A;Title: Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis</i> .
Db 250 TRQSGFQVSEEVNFNEDFNIDLEAECGTPCSDF 281			A;Reference number: A86141; MUID:21016719; PMID:11130712
			A;Accession: C86446
			A;Status: preliminary
			A;Molecule type: DNA
			A;Residues: 1-979 <STO>
			C;Cross-references: UNIPROT:Q9FVR3; GB:AE005172; NID:910801364; PID: AAC23436.1; GSPDB.GI
RESULT 3			C;Genetics: A;Map position: 1
T09074	semaphorin receptor VESPR - human		Query Match 3.8%; Score 103.5; DB 2; Length 979;
C;Species: Homo sapiens (man)			Best Local Similarity 21.2%; Pred. No. 5.2;
C;Accession: T09074	Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004		Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;
R;Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; F			A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and bi
Immunity, 8, 473-483, 1998			A;Reference number: Z16555; MUID:98246049; PMID:9586637

342	ERKWHAKVKBEDQIKRPRAL---VAPKATWMSDGT---HNFGTAWSGPPIHSGRDHASV	396	Qy	267 PDVDESSRSI FEYTRIEDLDP SKVTSMSA VFTPLPTCLOHRS CDA CMSSDLT FNSWCH 326	
Db			Db	326 ADVGEQPGVG YGS SPAAE APPSKS PMSL	-NQTWPE 361
64	SQDL-----GGT LAMD	105	Qy	327 VLQRCS SGFD RQEWMDYCG A QAE GRM CEDF QDEDH DSA SP DTS	-372
Db	TLPDN RTRVVEDDMH SYYVSRL YLG PSEPHSR	446	Db	362 LNQS -----SEWE TIS -ERS SSS QQT QF -DS NIA PA P DPT I VHP VPI RMPSK I 411	
397	I QVLLDPGDBPVE GKG GEG GRAD LEV DIRP	105	Qy	373 -----FS PYDG DLT TSS SFL FDS LTT EDDT KLN P	-414
106	BLWDVAEANESQVKHTILSNTNTHQASR VVTLSPDFPFYGHPLR QTIAT GOF I PFG bVI	165	Qy	-----YAGGD GLQ NNL S	-414
447	K-----AGM AVAL YRA SAIM SN-----GPFI LNLD CDH YVNSRAF --RGIC FMDHD	493	Db	412 HMQEMEL KRT SS DHTN P TSP LLVK PDS DSE BNK NS SVK FES GNT DVGS SDF PSD	--469
166	H RMLT ATQY-----VAPLMANF NG PGS D	195	Qy	415 PTK GGPV -----HL GT	426
494	GDRVSTVQFPDP RFEGIDPSSD YAN KNTVFF DNL ALD GIG PPM YVGT GCL P RRT AL YGP	553	Db	470 PEQG SSV TQR SHSG T	486
196	DNGTYFVV OMHDHV YLQ WED KGS FTOA AL LH DGRIV FAYKE I PMSV --PEI SSO QHP-	251			
554	NPPD FVFE-----EPPG S YCP-----LICK RSP TAVASE PYYT DED BDR	595			
252	-----VKT GLS DAF M LNP S DVP BES RRS FPE YH -RIEL D P SKV T-SMA VEF TPL PT	303			
596	F DIG LIR KQF PSS SMLVN -SYK VAA EFG RPL AT VASS RSL RGP PGS LTGS RKP LD FAT VNE	654			
304	C LOHRS CDA MG S DLT FNC S WCH -V LQ R C S S G F D P Y Q E WMD Y G C A Q E A E	352			
655	A VNV TSC WYB DKTE WFG FEN VGH YGS VTED VV TGF RME HEK G VRS F YCV TEP D	705			
RESULT 6					
383345					
hypothetical protein F16F4.9 - Arabidopsis thaliana					
C.Species: Arabidopsis thaliana (mouse ear cress)					
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004					
R.Theology: A; Becker, J.R.; Palm, C.J.; Federeriel, N.A.; Kaul, S.; White, O.					
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Davis, R.W.					
ansen, N.F.; Hughes, B.; Huizar, L.					
Nature 408, 816-820, 2000					
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Ropson, C.; Khan, S.; Khaykin, E.					
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; M.					
Rizzo, M.; Poone, T.; Rowley, D.; Saraco, H.					
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;					
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.					
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.					
A;Reference number: A86141; MUID:21016719; PMID:11130712					
A;Status: preliminary					
A;Molecule type: DNA					
A;Residues: 1-733 <STO>					
A;Cross references: UNIPROT:Q9LMN7; GB:AE005172; NID:98920637; PIDN:AAF81359.1;					
C;Genetics:					
A;Map Position: 1					
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO					
Query Match 3.8%; Score 101; DB 2; Length 733;					
Best Local Similarity 24.1%; Pred. No. 5.5;					
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;					
Qy 257 SD AFM I NPS P D P F E S R R S I -----F E Y H R I E L D P S K T S M S A V E -F T P I P T C L 305					
Db 139 STG C M S L C D T P P E N S K C N G V G C C R T E V S I P L D S H R I E T O P S R F E M T S Y V E H F N P -----193					
Qy 306 Q H R S C D -A C M S S D I T F N C S -----W C H V L Q R C -----SS 333					
Db 194 ---C S Y A F V B U C M F M N S S L E D I K D L R V T R F P V L D D I G N Q T C V V G R N I C C G N S T 249					
Qy 334 G F D R Y Q E W M D Y C G A Q E G R M -----C R D F Q D -E D H D S A S P D T -----S F -S P Y 376					
Db 250 C P D S T R G Y N C K Q L G Q P D Y N P Y L S D G C O D I N E C T R I N C S D T C E N T I G S F H Q C Q P S 309					
Qy 377 D G L I T T E S S S L F I D S L I T E D D T K N P Y A G D G L O N N S P Y T K G -T P V H L G T I V G V I A V L 435					
Db 310 G S D I N T R M S C -I D T P R K S E -----P C Y L G W N T V L L G T T I G F J I L L 349					
Qy 436 L V A A I 440					
Db 350 T I S Y I 354					
Qy 233 -O R Q V V N O F K T I Q P D L N G F L G G -----S A A K E F T K S K L P I L S H I W E L S D 279					
Db 213 W E D K G S F T -F Q A A L H H D R I V P A Y K -----E I P M S V P E I S S Q H P V K T G L D A F M I L N P S 266					
Qy 280 R D K G A L T I D E F C A F H -----L I V V A R K N G T D I P E K P E -----S I M P K I D I E S 325					
RESULT 7					
S1.8606					
C.Species: Rhizobium sp.					
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003					

C;Accession: S18606 R;Oteras, M.; Finan, T.M.; Stanley, J. Mol. Gen. Genet. 230, 257-266, 1991	C;Superfamily: phosphoenolpyruvate carboxykinase [ATP] C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop C;Keywords: carbon-carbon lyase; nucleotide binding motif A (P-loop)
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-535 <OST>	Query Match Score 3.7%; DB 2; Length 535; Best Local Similarity 19.8%; Pred. No. 4.3%; Matches 71; Conservative 50; Mismatches 157; Indels 80; Gaps 15;
Qy 11 VLRBRARALSPQAGHDEPGSMWAARKTGTVRGNRRAESPGHIV--SEPDRTQLSQDLG 68 Db 17 VFPFLGRSLQRLRAELEYE ---AFARRGALTAGCALCARTGQTGSPKDKTVVRDAAT 72	Qy 69 GGTIAMDT---LDDNTRRVVED----NHSYVYVSRLYGPSPHSRELWVDYAEANRSQ 118 Db 73 GDQIWDNNSAISENFERLQDMIAHKGMSTVQDLVYAGAQGK----CYADARRH 127
Qy 119 VKIHTI-LSNTHRQASRVVLS-----FDFP-FYGH-----LHQITTA 154 Db 128 IRWHLSLFIRMLLIRPPREGLASFLPKLTIDLPSEFKANPERHGCRGETTIACDITKGVL 187	Qy 155 TGGTFMGDYTHRMILTATQVAP-----LMANFNPGYSDNSTVVYP-----195 Db 188 IGGTSYAGEMIKSVETVNLNYLLPKAVMPMPHCSSANGPAA---GITAIFFGLSGTGKTTL 244
Qy 196 -DNGCTVFFVQWDHYLQLOGMEDKGSEFTFOQALHHGRIIVPAYKEPMVSPEISSLQQHPVKT 254 Db 245 ADPNRTLIGDDEH---GNSDKGVENFEQG----GCYACAAIRLSEAEEPIPATTRRFET 295	Qy 255 GLSDFAMLNPSDPVYPPERSRSRISFYHRFIELDPSKVTMSAVETTPPLPCLQHRSICDA 312 Db 296 VMENVVLDERRAPDFDNG---SLTENTRAYPLDFIPNASETGAPQPTTILMTADA 350
RESULT 8	
hypothetical protein DKFZp434P113.1 - human (fragment)	
C;Species: Homo sapiens (man) C;Accession: T12529 C;Status: preliminary A;Molecule type: RNA A;Residues: 1-113 <WAM> A;Cross-references: UNIPROT:Q9UG37; ENSEMBL:AL080145 A;Experimental source: adult testis; Clone DKFZp434P113 C;Genetics: A;Note: DKFZp434P113.1	Query Match Score 3.7%; DB 2; Length 113; Best Local Similarity 23.0%; Pred. No. 15; Matches 67; Conservative 37; Mismatches 119; Indels 68; Gaps 16;
Qy 162 GDVFRHMLTATQYAPLMANFNPGYSDNSTVYTFDNGTYFVVOQDHVYLOG--WE----214 Db 823 GDIAH---IVDIQTNQKLLTFNPDIANN---YRNRCATENPTDVLVNDGVLMDVRSAQ 876	Qy 215 ----DKGSFTFOQALHHGRIIVPAYKEI-----PNSVPEISSLQ---HPVKTGLSD 258 Db 877 AIHKDFKFNINNISGQVFHFNPLEVINTEWDLQRFLHHTVPAIDQCRVVFENNTGTVNYG 936

Qy	259	AFMINTNPSPDVPESSRRSIFIFYHRIELDPSKTSVMSMAVEFPLPTC-LQHRSQDACHMSSD	317
Db	937	AMQLADDDELMEERMKNSPFF-----GSSFRFTNFDYKPIATIDVKRNIFDLCTD-	986
Qy	318	LTFNCSWCHYLQRCSGGFDYRQEWNMDYGC-----AQAEGRGMCEDFDQEDH	364
Db	987	-TKDC-YLAVENQGS-AMDALN--MTDVCRLEYVERQRQLAEDDEDEEQEEEQEEDD	1040
Qy	365	DSASPDTSFSFYDGDILTTSSSLFIDSLLTETDDTKLNPYAGGDSLQNLNLP	415
Db	1041	DEDDDDT-D----DLDLDTDQLEALEBEDDN--NENAGSDG-DNDFSP	1082
.			
RESULT 9			
T16074	hypothetical protein F14B8.6 - Caenorhabditis elegans		
C;Species:	Caenorhabditis elegans		
C;Date:	20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004		
C;Accession:	T16074		
R;Geisel, C.			
Submitted to the EMBL Data Library, June 1995			
A;Description: The sequence of <i>C. elegans</i> cosmid F14B8.			
A;Reference number: Z18456			
A;Accession: T16074			
A;Status: Preliminary; translated from GB/EMBL/DDJB			
A;Molecule type: DNA			
A;Residues: 1-345 <GEI>			
A;Cross-references: UNIPROT:Q19446; EMBL:U28737; PID:g860723; PIDN: A;Experimental source: strain Bristol N2			
C;Genetics:			
A;Gene: CESKR-F14B8.6			
A;Introns: 17/3; 61/2; 93/3; 144/2; 197/1; 218/3; 255/2; 327/3			
Query Match	3.6%	Score 98;	DB 2;
Best Local Similarity	18.7%	Pred. No. 3.4;	Length 345;
Matches	50;	Conservative	46;
		Mismatches	95;
		Indels	76;
		Gaps	12;
Qy	240	MSVPRISSQQHPVKTGCLDAFMILNPSDPVESPERRSSIFEYHRIELDPSKUTSMSAVEFT	299
Db	96	ISVSGTATMRCATLGNAASDSTLMTOQSNSQDNRNNQ-----TPIQVTS-NTNGWT	145
Qy	300	PLPTCQHPSDACKNSDLFNFNCWSHVFLQRCSSGFPRQEWMDYGAQEAEGRMCDF	359
Db	146	LTATI-NRKNCG-ADQYGFNCN---EQCST---VNVNDYYCYTCGNSNGOKTCACAS-	191
Qy	360	QDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLLTEDTKLNPYAGGDSLQNLNLSPKTPKG	419
Db	192	-----GDVNPD-DCSVDHPIISTWNSP-----NTQCSASALEN	222
Qy	420	TPVHLGTTIVGIVLVLVAAIL---AGTY-----INGHPTTSNALFF	459
Db	223	TYFWLMSFAIIIAILILILVLLBLCCGFLFTGRQSARRSSEGDWVVPKTKANHELYD	282
Qy	460	IERRPHWPMKFRSHDHSYAEVP	486
Db	283	ADITPHH---QYRRHQDNNSGESTP	306
.			
RESULT 10			
S45429	probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)		
N;Alternate names: hypothetical protein YBL079w			
C;Species:	Saccharomyces cerevisiae		
C;Date:	09-Jun-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004		
C;Accession:	S45429; S45420; S45815; S59226		
R;Obermaier, B.; Gassnerhuber, J.; Piravendan, E.; Domdey, H.			
Submitted to the EMBL Data Library, May 1994			
A;Description: Sequence analysis of a 78.6 kb segment of the left end of Saccar			
A;Reference number: S45429			
A;Accession: S45429			
A;Molecule type: DNA			
A;Residues: 1-1502 <OE>			
A;Cross-references: UNIPROT:P31181; EMBL:X79489; PID:g466661; PID:g9496702			

A;Experimental source: strain S288C
R;Domdey, H.; Gassenhuber, J.; Piravandi, E.
A;Reference number: S45816
A;Accession: S45820
A;Molecule type: DNA
A;Residues: 1-1502 <DOM>
A;Cross-references: EMBL:Z35840; NID:9536126; PID:g536127; MIPS:YBL079w
R;Contreras, R.; Piers, W.; Logghe, M.; Moilemans, F.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45802
A;Accession: S45815
A;Molecule type: DNA
A;Residues: 1262-1502 <CON>
A;Cross-references: EMBL:Z35840; MIPS:YBL079w
A;Experimental source: strain S288C
R;Gassenhuber, J.; Domdey, H.
Year: 11, 1103-1112, 1995
A;Title: Sequence analysis of a 78.6 kb segment of the left end of *Saccharomyces cerevisiae*
A;Accession: S59226
A;Status: nucleic acid sequence not shown; translation not shown
A;Map position: 2L
A;Molecule type: DNA
A;Residues: 1-1502 <CON>
A;Cross-references: EMBL:X79489; NID:9496661; PID:CAA56029.1; PID:g496702
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C;Genetic CS:
A;Gene: SGD:NP_170
A;Cross-references: SGD:S0000175; MIPS:YBL079w
A;Map position: 2L
C;Keywords: nucleus; transmembrane protein
F;431-24/7/Domain: transmembrane #status predicted <TM1>
F;434-45/0/Domain: transmembrane #status predicted <TM2>
F;764-780/Domain: transmembrane #status predicted <TM3>
F;1311-1327/Domain: transmembrane #status predicted <TM4>
F;1382-1399/Domain: transmembrane #status predicted <TM5>
F;1406-1423/Domain: transmembrane #status predicted <TM6>

Query Match 3.6%; Score 98; DB 2; Length 1502;
Best Local Similarity 22.7%; Pred. No. 26;
Matches 62; Conservative 41; Indels 64; Gaps 14;

Qy 61 TQLQDGGTLANDTLPNRTRVVEDNFSYYNSRLYGSSEPHSRELWVDAANRSQVK 120
Db 778 TRLLRDIVSRHVFVN-TFTTNRV---TSHAFTSS--DFITPSINNLKSDELQRNRII- 829
Qy 121 IHTILSNTRHQASRVVLSFD-FPYGHPLPQRIITATGGPFMDVIRHMLTATQYVAT-L 178
Db 830 -----SKVSIISDCEIYV---ISSINILNEFFITYGDSDI----SQISAYV 868
Qy 179 MANNPNGTSNDSTVYFD-----NGTTFVYVQDHYVILQGWEDKGSPFOAALHHHDGR 231
Db 869 LANNNSNQRIDKTEBVANQAEASTAINAMKMQV-----3IKEGSIISFLAVLYEESEV 919
Qy 232 -----VFAFYKEIPMSVPBIISSOHPVKTGLSDAFMILNPSDVPESSRRSIFPEYHRTEL 285
Db 920 EGFDNQYLGFKDI-1SFVSLDVQDKLVKIDFKOLF-----APNDKTKSLIREILISI 970
Qy 286 DPKSVTMSMAVEFPPLPTLQHRSACDMSSL 318
Db 971 INRNNTKGASIEYT-ATPLQERCGSFCASDI 1001

RESULT 11
IB1196 NEJD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
Db 916682/Domain: Ubiquitin-protein ligase homology <UBI>
A;Gene: NEJD-4
C;Protein family: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin-protein ligase homology <UBI>
A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetic CS:
A;Molecule type: mRNA
A;Residues: 1-397 <SCR1>
A;Accession: S43740
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:g298114; PID:92981
A;Molecule type: protein
A;Residues: 23-40 <SCR2>
C;Superfamily: Serpin

RESULT 12
IB1196 NEJD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: S33415; S43740
C;Cross-references: R;Scrocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.
Endocrinology 132, 903-909, 1993
A;Title: Spatial and temporal distribution of corticosteroid-binding globulin and its me
A;Reference number: S33415; MUID:9145908; PMID:7916682
A;Accession: S33415
A;Molecule type: mRNA
A;Cross-references: 1-397 <SCR1>
A;Accession: S43740
A;Molecule type: protein
A;Residues: 23-40 <SCR2>
C;Superfamily: Serpin

RESULT 13
IB1196 NEJD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: 183196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression

C;Keywords: Glycoprotein; steroid binding E1-22/Domain: signal sequence #status predicted <SIC> E1-3-39/Product: corticosteroid-binding globulin #status experimental <MAT> P;39,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted	Qy 3.6%; Score 96.5; DB 2; Length 397; Best Local Similarity 20.2%; Pred. No. 5.5; Matches 33; Conservative 47; Mismatches 104; Indels 59; Gaps 11;	Db 302 P 302 586 P 586
Query Match 61 TQLSDLGCGTLMNDTLPLDNRTRVVEDNHSYYVVERLYGSEPHSRELWVDAE-----A 114 Best Local Similarity 20.1%; Pred. No. 5.5; Matches 33; Conservative 47; Mismatches 104; Indels 59; Gaps 11;	RESULT 14 Qy 61 TQLSDLGCGTLMNDTLPLDNRTRVVEDNHSYYVVERLYGSEPHSRELWVDAE-----A 114 Db 114 TGLEMMAGTMFELLNLKEDSFELADTKYYESEALTISKD----WTKAGEQINNTVK 168 Qy 115 NRSOVKIHTILSNTHROASRVLSDFD-----PEYGHPLRQITIACTGGIFMGDVTHR 167 Db 169 NKTQKIEHVSDLSSATILINYFLKGIWKLPLFSPTNTE-----EDYV 216 Qy 168 MLTAQTYVAPLMANPNPGTSNDNSTV-----YFDNGTVFVQWQDAVYLOGMEDKGSFT 220 Db 217 NETSVKVPMMVQSGNISIERTDSAIPCQMVQMVYVGNGTTFILPD---QGMQD----T 268 Qy 2221 FQAAQHHD----GRIVFAKEIPIMSVPIESSOH-----PVRTGLSSDAFMILNPSPV 269 Db 269 VVAALNRDIDTRWGKLMIP-RQMLYIPEKFSMSDTYDLDVLAvgIKDLFTNQSDADT 327 Qy 270 PESRRRSIPEYHR--IEUDPSKY 290 Db 328 TKDTPLTLTVLHKAMIQLDGKVN 350	Db 571480 Accession: S71480 Status: preliminary A;Molecule type: mRNA A;Residues: 1-399 <SCO> A;Cross-references: UNIPROT:P23682; EMBL:X74506; PIDN:CA52613.1; PID:94437 C;Genetics: A;Gene: Hox-B3 C;Superfamily: homeotic protein Hox B3; homeobox homology C;Keywords: DNA binding; homeobox; nucleic acid; transcription regulation F;160-216/Domain: homeobox homology <HOX>
Query Match 94 STTSSNSIIPSOSAKYPRVKEPSVQTP-SLKQIPQPMKESRQNQKSSSPSTETSGCERT 152 Best Local Similarity 20.5%; Pred. No. 6.7; Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;	Db 246 SSSOPPKVKGGLSDAFMILNPSPDVPESSRSIFBYHRIELDPSKVTSM-----AVEFT 299 Qy 94 STTSSNSIIPSOSAKYPRVKEPSVQTP-SLKQIPQPMKESRQNQKSSSPSTETSGCERT 152 Db 300 PLPRLCQLRSCDCADMSSDLT-----FNCWSCH-----VLQRQCSSGFDRYQEN-----M 343 Qy 153 PPGSASKHARTAVTSAQVELLEKEFHFNRYLCRPRVEMANLNLNSERQIKWFQNRRM 212 Db 344 DYGGAQEAEGRMCFQDEDDHDSASPDTSFSP-----YDGDLTTTSSSLFDTSLT 394 Qy 395 BDDTKLNPYAGGDLQNNL-----SPKTKGTPVHLGT 426 Db 213 KYKKDQKSKGM-----GSSSCGPSPTRGSPPPQPMQSSAGFMNALHTMISSNTDAPSPPS 264 Qy 427 IVGIVLAVLVAAILLAGTYINGHTPSNNAFLFERRPHWPANKFRSHPDHSTYAEVEP 486 Db 324 -----GNYVDSLPTSGFSLYGLNHLPHQAA-----NMDDYSGPPQMPPP 361 Qy 487 SGH 489 Db 362 SQH 364	Db 571480 Accession: S71480 Status: preliminary A;Molecule type: mRNA A;Residues: 1-679 <WIL> A;Cross-references: UNIPROT:Q09495; EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C34C12 C;Genetics: A;Gene: CESP; C34C12.2 A;Map position: 3 A;Intron: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3 Qy 16 ARAISPOPGAGHDEGPGSWAAGKTVRGNNRARESPGHYSSEPORTQSLQGGTLAMD 75 Best Local Similarity 23.3%; Pred. No. 1.2; Matches 36; Mismatches 130; Indels 65; Gaps 12;
Query Match 337 AKYLPKDQPTSSACYKPYFESTSSSSRKPKTASP-----PPBPTQISDQLANTGEVRY- 392 Best Local Similarity 20.1%; Pred. No. 5.5; Matches 33; Conservative 47; Mismatches 104; Indels 59; Gaps 11;	RESULT 15 Db 337 AKYLPKDQPTSSACYKPYFESTSSSSRKPKTASP-----PPBPTQISDQLANTGEVRY- 392 Qy 76 TLPDNRTRVVEDNHSYYVVERLYGSEPHSRELWVDAEANRSQ--VKTHTLISNTHROA 132 Db 393 -----WVNSGRPFNS----SESNSRNLLKIPGYKRPEPYIKEBGFITSASYKQ 439 Qy 133 SRVVL-SDFPPYGHPLRQITAT-----GGFIFMGDVTHRMILTATQVAPIMANENCY 186 Db 440 SEGMSF-----LKTGSATPNSKSAHFMDPDI-----SSTPYSHVVESENIN 486 Qy 187 SDNSTVVVF----DNGTVFVQWQDHVYLOGMEDKGSPFQOALNHHDGRIVPAYKEIIMS 241 Db 487 SSSPTGPPSEKDDNGAL-----GSOKSPMPDIALHN---IEDEKEYVOS 531 Qy 242 VPEISSQQHVVKTGLSDAFMILNPSPPDVPSRRSISFETHRIELDPSKTVTMSMATEFTL 301 Db 532 SSTGSSAPPENSKSDHF----DMFDISSTLYSRVE--PISSSSGGSTTSAPRYVK 585	Db 570642 Accession: S70642 Status: fragment C;Species: Rattus norvegicus (Norway rat) C;Sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S70642 R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. EMBO J. 15, 2371-380, 1996 A;Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na (+) A;Accession: S70642 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-887 <STA> A;Cross-references: UNIPROT:Q62940; EMBL:U50842; PIDN:91291646; PMID:8665844 C;Genetics: A;Gene: Nedd4 C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui

F;54-167/Domain: protein kinase C C2 region homology <KC2>
 F;246-283/Domain: WW repeat homology <WW1>
 F;402-439/Domain: WW repeat homology <WW2>
 F;559-496/Domain: WW repeat homology <WW3>
 F;555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match	Score	DB	Length
Best Local Similarity	3.5%	2	887
Matches	93	20	
Conservative	55	Mismatches	155
		Indels	181
		Gaps	25

Qy 14 EAARALSP-----OPGAG----HDEGPQ---SGWAARKCTVRG-----WNR 47
 Db 218 DQABELEPGRMVLLQDPAATHLQHPPPEPSPLPPGMWEERQDVGLRTRYVNHESRTTQWKRP 277

Qy 48 ARES-----PGHVSEPDRTOLSQLGGCTLANDTLPDNRTR-----VVEDNH 89
 Db 278 SPEDDLTDENGDIQLQAGAFTTRQRQISBDVPG-----PNHESSENWBIVREBZN 329

Qy 90 SYYYSR-LYGPSEPHSRELWVDVAEANRQSVKHTILSNTHRQASRVVLSDFPPYGHPL 148
 Db 330 TIVSQAVQSPSPGP-DIVQRLAE-----ELDTRLT-----MYGNPA 366

Qy 149 RQITATGGPIMGDVIFHMLTATQYALM----ANFPGY----SDNISTVYVFDNNTV 200
 Db 367 TSQPVTTSSNHSSRGCSSQTCIFEEOPTLVLLPTTSGLPGWEEKQDDRGRSYYVDINSK 426

Qy 201 FVVOWDHVYLQ-----GWEDKGSFTFOQAALHHGR1YF 233
 Db 427 -TTTWSKPMQDDPRSKIDAHLRGKTPVTDNSDLQPLPPWEEER-----THTDGRV/F 477

Qy 234 AYKEIPMSYPEISSLSSQHPVKTKGLSDAFM1LNPSDVPESR-RRSIFEVHFIELDPSKVTS 292
 Db 478 INHNIIKKTOWEDPRNQNAVITG-----PAEPYSDYRKYEFRRKLKKQ---522

Qy 293 MSAVEFTPPTCLOHRSACAMSSDLTFCMSWCHVLQROSSGFDRYOBMDYGAQBAE 352
 Db 523 -----TDLPNKPFEMK-----LRAANILEDSYRR-IMGYKRADELK 556

Qy 353 GRMCBDFQDB---DHDSAPD-----TSFSPYDGDLTTSSSLFIDSLLTDDT-KLN 401
 Db 557 ARLMIEFDGEKGLDYGGVAREWFFFLISKEMFNPYG-----LFETYSATEDNYLQIN 608

Qy 402 PYAG 405
 Db 609 PNSG 612

Search completed: November 3, 2005, 20:51:20
 Job time : 44 SECs

THIS PAGE BLANK (USPTO)